

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 12, 2006, 06:19:19 ; Search time 37.5 Seconds  
(without alignments)  
11469.038 Million cell updates/sec

Title: US-10-782-570-1  
Perfect score: 3939  
Sequence: 1 gtgaatcaataataataa.....caaatatgatattgattaa 2235

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frames\_n2p.model -DEV=xlp  
-Q/cgn2\_1/USPTO.spool\_p/US10782570/runat\_12012006\_060222\_7522/app\_query.fasta\_1.2375  
-DB=PIR -QFMT=fastan -SUPFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10782570 @CN 1 1 57 @runat\_12012006\_060222\_7522 -NCPUS=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80.4

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1159	29.4	1180	2	A26858
2	1158	29.4	1180	2	I39870
3	923.5	23.4	934	2	B29838
4	819	20.8	1136	1	US8881
5	706	17.9	659	2	S10228
6	691	17.5	652	2	I39811
7	688	17.5	1138	2	A48944
8	672	17.1	1160	2	I40589
9	655.5	16.6	1157	1	S49247
10	616.5	15.7	652	2	A27323
11	607	15.4	1228	2	S00873
12	588.5	14.9	719	2	I39815
13	585.5	14.9	719	2	I39814
14	585.5	14.9	719	2	S25383

15	576	14.6	1165	2	S11446	parasporal crystal
16	575	14.6	1178	1	USBSXH	parasporal crystal
17	574	14.6	649	1	JH0261	parasporal crystal
18	563.5	14.3	719	2	I40590	cry465 protein
19	562.5	14.3	1177	2	A49785	parasporal crystal
20	551	14.0	1154	2	S39536	parasporal crystal
21	540.5	13.7	1171	2	A37829	parasporal crystal
22	540.5	13.7	1171	2	I40572	parasporal crystal
23	538	13.7	1174	2	S32649	parasporal crystal
24	534.5	13.6	1176	2	A48970	parasporal crystal
25	530	13.5	618	2	S11445	parasporal crystal
26	526.5	13.4	655	2	S04140	protoxin - Bacilli
27	522.5	13.3	823	2	JC4181	parasporal crystal
28	519.5	13.2	1174	2	A42459	parasporal crystal
29	517.5	13.1	1160	2	S32647	parasporal crystal
30	514.5	13.1	1189	2	S00944	parasporal crystal
31	512	13.0	934	2	A2798	parasporal crystal
32	512	13.0	1176	2	JT0241	parasporal crystal
33	506	12.8	1176	2	JC2219	parasporal crystal
34	504	12.8	1172	2	S32689	parasporal crystal
35	502.5	12.8	1155	2	I39838	parasporal crystal
36	501	12.7	1176	2	A22617	parasporal crystal
37	501	12.7	1176	2	S02215	parasporal crystal
38	500	12.7	1156	2	S19306	parasporal crystal
39	491.5	12.5	1155	2	A26513	parasporal crystal
40	491.5	12.5	1155	2	JU0002	parasporal crystal
41	491.5	12.5	1156	2	A29125	parasporal crystal
42	491	12.5	1166	2	S32645	parasporal crystal
43	490.5	12.5	1155	2	S02134	parasporal crystal
44	486.5	12.4	1181	2	A41052	parasporal crystal
45	469.5	11.9	613	2	JC6033	mosquitocidal prot

## ALIGNMENTS

### RESULT 1

A26858  
parasporal crystal protein cry4Aa1 - Bacillus thuringiensis subsp. israelensis  
N:Alternate names: parasporal crystal protein cryIVA  
C:Species: Bacillus thuringiensis subsp. israelensis  
C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004  
C:Accession: A26858; S48691  
R:Ward, B.S.; Ellar, D.J.  
Nucleic Acids Res. 15, 7195, 1987  
A>Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding  
A:Reference number: A26858; MUID:88015571; PMID:2821500  
A:Accession: A26858  
A:Molecule type: DNA  
A:Residues: 1-1180 <WAR>  
A:Cross-references: UNIPROT:P16480; UNIPARC:UPI000016EA42; GB:Y00423; NID:G40351; PIDN:  
A>Note: the authors translated the codon GCA for residue 308 as Thr  
R:Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.  
FEBS Lett. 348, 249-254, 1994  
A>Title: Functional analysis of block 5, one of the highly conserved amino acid sequencer  
A:Reference number: S48691; MUID:94307434; PMID:7913448  
A:Accession: S48691  
A:Molecule type: DNA  
A:Residues: 667-676 <NIS>  
A:Cross-references: UNIPARC:UPI000017819A  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Alignment Scores:	5.5e-68	Length:	1180
Pred. No.:	1159.00	Matches:	283
Score:	54.55%	Conservative:	131
Percent Similarity:	37.29%	Mismatches:	281
Best Local Similarity:	29.42%	Indels:	64
Query Match:	2	Gaps:	25
DB:			

US-10-782-570-1 (1-2235) x A26858 (1-1180)

QY 13 AATAATAATGAATATGAGATTATCGATTCA-----AAGAAATTATCTTATCCTCTTAAC 66

db	6	AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn	25
Qy	67	AGAAATATTGATCATCTAGATACCCCTTACACAATAATCCAAATACCAATACCAATACCAAAAC	126
Db	26	-----TyrThrArgTyrProIleGluAsnSerProLysGlnLeuLeuGlnSer	41
Qy	127	ACAAATTACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGAATAATTC	186
Db	42	ThrAsnTyrLysAspTyrLeuAsnMetCysGlnGlnAsnGlnTyrGlyGlyAspPhe	61
Qy	187	GAGACATTGGCTAGTGTGATACAAATTTGCTGCAGTTAGTCAGGTACTATTGTATCCGGT	246
Db	62	GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValValGly	78
Qy	247	ACTCTGTTAGCGGTATAGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGGT	306
Db	79	ThrValLeuThrGlyPheGlyPheThrThr-----ProLeuGlyLeu-----	92
Qy	307	GCTATAATAATATCTTTTGGTACCTCAATCACTGTCTTTTGGCCGGGAGAACAAAGAC	366
Db	93	---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer	111
Qy	367	AAACAGTATGGACACAATTTATTAATGGGAGAAATTTTGTGTGTATACACCGTTAAACA	426
Db	112	AsnThr---TyrSerAspPheIleThrGlnThrLysAsnIleIleLysLysGluIleAla	130
Qy	427	GAAGCATAAACACAGCTAAAGTTCACAACTTTAGNAGGATTTAGACAAATATTACAAGC	486
Db	131	SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr	150
Qy	487	TATAATACAGCATTAGATGATGGAGAAATTTAAAGACATCAAGCTCTGGATTACCA	546
Db	151	TyrHisAsnHisLeuLysThrTyrGlu-----AsnAsnProAsnProGln	165
Qy	547	CCATCATCAGCATTAACAACAGTCGCTTAAATACGATTTGAGAATGTTCCAC	606
Db	166	AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle	185
Qy	607	AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACTTGAAACTTATAAAACGCTA	660
Db	186	ProGlnLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu	205
Qy	661	TTACTACCTATTATTCGCAAGCTGCTAAATTTTCATTTAAATTTATTACAAACAGGTGCT	720
Db	206	ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal	225
Qy	721	GAATGGCTGATGAATGGAATGCGAGATATACATCCTTCACAAATGGAACCTAATGCTGGGA	780
Db	226	LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro	244
Qy	781	ACATCAGATGACTATTATAAACTTTTAAAGAAAATATACCTAAATATAGTAACTATTGTT	840
Db	245	ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys	264
Qy	841	GCAAACTCTATAGAGAGGACTAAATAAACTTCGAAACGCAACCT-----	885
Db	265	ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp	284
Qy	886	---AATATGAGATGAGTATATTTAATGATTTATCGAAGATATATGACTATTTACTGTATTA	942
Db	285	GlyAsnIleAsnTyrAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu	304
Qy	943	GATACCTATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGA	1002
Db	305	AspValValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle-----	320
Qy	1003	ATAGTGGCATTAACACTGAACTTACAAGAGAAATTTATACAACTGGAATAAAATTTTGAC	1062
Db	321	-----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu	337
Qy	1063	CGTCTTACTTACCTTGAATTCACCCCAATCTCGGTATATATGGAATATATATTTAAACGGT	1122



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Db 524 HisSerSerValAspProIysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla 543
Qy 1699 ATCAAGGTAAACAGCTTTGATACAACTCTAAGGTAATTAAGAGGACCTGGTCATACAGGA 1758
Db 544 ValIysAlaAsnSerLeuGlyThrAlaSerIysValValGlnGlyProGlyHisThrGly 563
Qy 1759 GGAACTTGGTTTATTCAAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACCTCTTAAT 1818
Db 564 GlyAspLeuIle-----AspPheIysAspHisPheTyrIleThrCysGlnHisSerAsn 581
Qy 1819 TCTACACAATCTTATTACATAGCTTCGATACGCTACAAATGGTGGCGGAAATACTCTT 1878
Db 582 PheGlnGlnSerTyrPheIleargIleargTyrAlaSerAsnGlySerAlaSerThrArg 601
Qy 1879 CCTAATATATCTTCAATACCAAGAGTAAATAGGAATACCACCTCAACGACTCAACAAAC 1938
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu--GlyMetAlaLeuAsnPro 620
Qy 1939 ACTTTTCTGGTACAAATTAATTAATTTACATACGAGATTTTGGGTATTTTCCAATTT 1998
Db 621 ThrPheSerGlyThrAspTyrThrAsnLeuIysTyrIysAspPheGlnTyrLeuGluPhe 640
Qy 1999 CCAAGTCAGTAACATTAACCTTTAAATCGAAACATACCATTATATATTTAATCGTCAGAT 2058
Db 641 SerAsnGluValIysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
Qy 2059 GTA---TCAAAATTAATTCATTCATGATAAATTTGAATTTATACCAATTAATTCCTCT 2115
Db 661 ValTyrThrAsnThrThrValLeuIleAspIysIleGluPheLeuProIleThrArgSer 680
Qy 2116 GTAGCCAAATAGAGAAACAAATTAAGAACTATCCAAACAAATTAATTAATTAATTT 2175
Db 681 IleArgGluAspArgGluIysLeuGluThrValGlnGlnIleAsnThrPhe 700
Qy 2176 TTCACAAATCATACAAATAACTTTAAATATAGAGGACACAACTATGATATTGAT 2232
Db 701 TyrAlaAsnProIleIysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsn 719

RESULT 3
B29838
paraaporal crystal protein - Bacillus thuringiensis subsp. israelensis (fragment)
C:Species: Bacillus thuringiensis subsp. israelensis
C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: B29838
R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wiid, M.; Walfield, A.M
J. Bacteriol. 166, 801-811, 1986
A:Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal
A:Reference number: A94672; MUID:86223796; PMID:3011746
A:Accession: B29838
A:Molecule type: DNA
A:Residues: 1-934 <DNA>
A:Cross-references: UNIPROT:P09662; UNIPARC:UPI00001781A0; GB:M12662; NID:g143228

Alignment Scores:
Pred. No.: 1,19e-52 Length: 934
Score: 923.50 Matches: 262
Percent Similarity: 47.26% Conservative: 117
Best Local Similarity: 32.67% Mismatches: 270
Query Match: 23.45% Indels: 153
DB: 2 Gaps: 34

US-10-782-570-1 (1-2235) x B29838 (1-934)
Qy 13 AATAATAATGAATGAGATTATCGATTCAAGAATTTATCTTATCTCTTCTTAACAGAAAT 72
Db 6 AsnIysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25
Qy 73 ATTGATCATCTTAGTACCTCTACCAATTAATCCAAATCAACCCATTCAAAAACAAAT 132
Db 26 -----TyrSerArgTyrProLeuAlaAsnIysProAsnGlnProLeuIysAsnThrAsn 43
Qy 133 TACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATATGGTGATAATTTTCGAGACA 192
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Db 44 TyrIysAspTrpLeuAsnValCysGlnAspAsnGlnGlnIleTyrGlyAsnAsnAlaGlyAsn 63
Qy 193 TTTGCTAGTGCTGATACAAATTCGTCAGGTACTAGTCAGGTACTATTGTATCCGGTACTCTG 252
Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83
Qy 253 TTAGCCCGTATAGTGGGCTCATTCTTATATCCGACCGATAGGAATAATATAGGTGCTATA 312
Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95
Qy 313 ATAATATCTTTTGTACCTTAATCAGCTGCTTTTGGCCGCGGAGAGAACAGACAAACA 372
Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp--GlnGlySerAspProAlaAsn 114
Qy 373 GTATGGACACAAATTTATTAATGGGAGAAATTTTGTGTATACACCGTTTAACAGAA--- 429
Db 115 ValTrpGlnAspLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
Qy 430 -----AGCATAAACAGCTTAAGTTACAACTTTAGAGGATTTAGACAAATATTACAA 483
Db 131 AspIysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
Qy 484 AGCTATAATACAGCATTAGATGATTGGAGAAAATTTAAAGAACTACAAGCTCTCGATT 543
Db 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163
Qy 544 CCACCATCATCAGCATTTACAAACAGCTGCTTGAATCTTAAATAACGATTTGAGAGATGTT 603
Db 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181
Qy 604 CACAAAT-----GATTTTATTCGAGAAATACCTGTTTCCAACTTGAACCTTATAAA 654
Db 182 IleAspIysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199
Qy 655 ACGCTATTACTACTTATTATGCGCAGCTGCTAAATTTTCATTTTAAATTTTATTATCAACA 714
Db 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216
Qy 715 GGTGCTGAATTTGGCTGATGAATGGAATGCAGATATACATCTTCCAAAATTTGAACCTAAT 774
Db 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
Qy 775 GCTGGAACATCAGATGATATATAAA---CTTTTAAAGAAATATATACCTTAATATAGT 831
Db 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253
Qy 832 AACTATTGTGCAATACCTATAGAGAGGACTAAATAAATTCGAAACGAACTTAATATG 891
Db 254 AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
Qy 892 AGATGGAGTATATTAAATGATATTCGAAGATATATGACTATTACTGTATTAGATCTATC 951
Db 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
Qy 952 GCTCAATTTCTTTTATGATATAAGAGAGATACAAAGATTCAAATGAGGAGAAATAGGTGC 1011
Db 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307
Qy 1012 ATTAAAACTGAACCTTACAGAGAAATTTATACAACTGAAATTAATTTTTCACCGCTTACT 1071
Db 308 ValIysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326
Qy 1072 TACCTTGAATTCACCCAAATCTCGCTAATATGAATATATTAATTAACACGTTTCAGGGCTT 1131
Db 327 -----ThrIleThrGluLeuAsnGlyLeuThrArgAsnPro--- 339
Qy 1132 AGATTATTTTCAATTTTAGATGAATTTATATATTTTATATACAAAAT----- 1176
Db 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359
Qy 1177 GAAACGCTAC-----GGGAATCGTTTACGTATGTTATGCGAATTCGTAAT 1218
::: |||
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Db 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373  
Qy 1219 AGATCTACTTATGCTACGACGAGTAAATTTATATATGAGAAAGACAGGT----- 1272  
Db 374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392  
Qy 1273 ---CCACCCACCAACAAACTTTTAAATCACTTTGAATCCTAT-----AAAGTT 1317  
Db 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412  
Qy 1318 TCAATTGTAAGTATGATGACAGTAAGTAACTCTACTCCCTTTTCCATAATATCTTTACA 1377  
Db 413 GluIleValArgHisArgGlu-----TySerAsp 422  
Qy 1378 ATTAATCAAAATGAACTTTTATTAATTAATTAATCACTAGTATAATAATTAACATATTCAGCT 1437  
Db 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441  
Qy 1438 GGGGGGAATTTATCTTAATCAATAAATAAACAACACTGATTTTCAATTTCTGTATAAAGAAC 1497  
Db 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461  
Qy 1498 TGTAACCAATTAATTAATCAAAATGTTTACCAAGCTATAATAGTTATAGTCATATTTTA 1557  
Db 462 TrpLys-----AsnGluGluTyrGlyHisThrLeu 471  
Qy 1558 TCCAGTCTTTCTTTATTTATTTATTTCTTATAAATTTGATTTAGCGCTAAATATATATAT 1617  
Db 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgLysArg 488  
Qy 1618 ACAGTGCTATTAGGATGACACACAGTATGTTTATAGAAATAATGCAATATTCAGATATA 1677  
Db 489 ArgValAlaPheSerTyrThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508  
Qy 1678 ATAATTCAATGATCCCGCAATCAAGGTAACTGTTGATACAACTCTTAAGTAAT 1737  
Db 509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528  
Qy 1738 GAAGGCTGCTCATACAGGAGGAACCTGTTTATTTTCAAAAGTCAGGCGGTTTAG 1797  
Db 529 LysGlyProGlyHisThrGlyGlyAspLeuValIleLeuLysAspSer-----MetAsp 546  
Qy 1798 ATTCATCATGAGA---ACTCCTAATTTCTACACATCTTATTATACATTTAGATTCGATCCGCT 1854  
Db 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566  
Qy 1855 ACAATGCTGCTGGAATATCTCTCTTAATATATCTTCTTACAAATACCGAGGTAAATAGA 1914  
Db 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581  
Qy 1915 ATACCACTCAACGACTCAACACACTTTTCTGTCACAAATTAAT-----AATTGA 1968  
Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600  
Qy 1969 CAATACGAGAGATTTGGGTATTTCCAAATTTCCAAAGTACAGTA----- 2010  
Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620  
Qy 2011 -----ACATTACCTTTAATCGAAACATACCATTTATATTTAATTCGTGCAGATGTA 2061  
Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635  
Qy 2062 TCAATTAATTTAATCATTTGATTAATTAATTTACCAATTTACCAATTTCTCTCTGTCGC 2121  
Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654  
Qy 2122 CAAATAGAGAAACAAATAATTTAGAACTATCCAA----- 2157  
Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674  
Qy 2158 -----ACAAAAATA----- 2166  
Db 675 AsnAsnLysValLeuThrIleLysIleAspSerMetAlaValLysAlaArgLysValVal 694

Qy 2167 AATACATTTTTCACAAATCATACAAATAACTTTTAAATATAGAACCCAAACTATGAT 2226  
Db 695 AsnProMetPheThrSerGlyAlaLysAsnArgLeuLysLeuGluThrThrAspTyrGlu 714  
Qy 2227 ATTGAT 2232  
Db 715 IleAsp 716  
RESULT 4  
USBS91  
paraesophageal crystal protein cry4Ba1 [validated] - Bacillus thuringiensis subsp. israeliensis  
N;Alternate names: delta-endotoxin Bt8; insecticidal protein ISRH3; mosquitoicidal 130K p  
C;Species: Bacillus thuringiensis subsp. israeliensis  
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 05-Oct-2004  
C;Accession: S003398; A37587; J70315; A28541; I39869; I40584  
R;Chungjatupornchai, W.; Hofste, H.; Seurinck, J.; Anguthanasombat, C.; Vaeck, M.  
Eur. J. Biochem. 173, 9-16, 1988  
A;Title: Common features of Bacillus thuringiensis toxins specific for Diptera and Lepid  
A;Reference number: S003398; MUID:88185334; PMID:2833395  
A;Accession: S003398  
A;Molecule type: DNA  
A;Residues: 1-1136 <CHU>  
A;Cross-references: UNIPROT:P05519; UNIPARC:UPI0000001B1D; EMBL:X07423; NID:G40353; PIDN  
R;Yamamoto, T.; Watkinson, I.A.; Kim, L.; Sage, M.V.; Stratton, R.; Akande, N.; Li, Y.;  
Gene 66, 107-120, 1988  
A;Title: Nucleotide sequence of the gene coding for a 130-kDa mosquitoicidal protein of B  
A;Reference number: J70315; MUID:88329719; PMID:2901387  
A;Accession: A37587  
A;Molecule type: DNA  
A;Residues: 1-50, 'D', 'S', '66-192, 'PHKCTRMVY', 202-204, 'C', 207-363, 'LVQIYLKPN', 374, '  
YKEPLEORLVQNVY', 573-593, 'N', 595-686, 'GITS', 691-720, 'R', 722-822, 'LIVSVSRCA', 833-835, 'WD'  
A;Cross-references: UNIPARC:UPI000016EA34; GB:M20242; NID:G142737; PIDN:AAA22337.1; PID:  
A;Accession: J70315  
A;Molecule type: protein  
A;Residues: 1-13 <YA2>  
A;Cross-references: UNIPARC:UPI00001747C0  
A;Note: the majority of sequence differences are consistent with frameshift errors  
R;Tungpradubkul, S.; Settassatien, C.; Panyim, S.  
Nucleic Acids Res. 16, 1637-1639, 1988  
A;Title: The complete nucleotide sequence of a 130 kDa mosquito-larvicidal delta-endotoxin  
A;Reference number: A28541; MUID:88157738; PMID:2831510  
A;Accession: A28541  
A;Molecule type: DNA  
A;Residues: 1-204, 'R', 206-1136 <TUN>  
A;Cross-references: UNIPARC:UPI000016EA3C; EMBL:X07082; NID:G40309; PIDN:CAA30114.1; PID  
R;Sen, K.; Honda, G.; Koyama, N.; Nishida, M.; Neki, A.; Sakai, H.; Himeno, M.; Komano,  
Agric. Biol. Chem. 52, 873-878, 1988  
A;Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes  
A;Reference number: I39869  
A;Accession: I39869  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-202, 'C', 205-271, 'L', 273-324, 'Y', 326-1136 <RES>  
A;Cross-references: UNIPARC:UPI0000156E4D; GB:D00247; NID:G216287; PIDN:BA00178.1; PID:  
R;Anguthanasombat, C.; Chungjatupornchai, W.; Kertbundit, S.; Luxanani, P.; Settassat  
Mol. Gen. Genet. 208, 384-389, 1987  
A;Title: Cloning and expression of 130-kd mosquito-larvicidal delta-endotoxin gene of Ba  
A;Reference number: I40584; MUID:88038331; PMID:2890080  
A;Accession: I40584  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-142 <RE2>  
A;Cross-references: UNIPARC:UPI000016EA41; EMBL:X05692; NID:G40350; PIDN:CAA29174.1; PID  
C;Comment: This protein is toxic to many lepidopteran larvae.  
C;Superfamily: Parasporal crystal protein  
C;Keywords: delta-endotoxin  
Alignment Scores: 7.61e-46 Length: 1136  
Pred. No.: 819.00 Matches: 246  
Score: 47.70% Conservative: 117  
Percent Similarity: 32.33% Mismatches: 268  
Best Local Similarity:











C,Keywords: delta-endotoxin

Alignment Scores:	2.85e-36	Length:	1160
Pred. No.:	672.00	Matches:	216
Score:	43.24%	Conservative:	123
Best Local Similarity:	27.55%	Mismatches:	317
Query Match:	17.06%	Indels:	128
DB:	2	Gaps:	29

US-10-782-570-1 (1-2235) x 140589 (1-1160)

Qy	1	GTGAATCAAAATAATAAATGAATATGAGATATCGATTTCGATTCAAAGAAATTTATCTTATCCT	60
Db	1	MetSerProAsnAsnGlnAsnGluTyrgluileileaspAlaLeuSerProThrSerVal	20
Qy	61	TCTAAGAGAAATATTGATCATTTCTAGATACCTTTACACAAATAATCCAAATCAACCAATTA	120
Db	21	SerAspAsnSerIle-----ArgTyrProLeuAlaAsnAspGlnThrAsnThrLeu	37
Qy	121	CAAAACACAAATTAACAAGAGTGGCTCAATATGTGTCAAGG---AATACACAAATATGGT	177
Db	38	GlnAsnMetAsnTyrLysAspTyrLeuLysMetThrGluSerThrAsnAlaGluLeuSer	57
Qy	178	GATAATTTCCGAGACATTTGCTAGTGTCTGATACAAATTCGTGAGTTAGTGCAGGTACTATT	237
Db	58	ArgAsnProGlyThrPheIleSerAlaGlnAsp-----AlaValGlyThrGlyIleasp	75
Qy	238	GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGCATAGA	297
Db	76	IleValSerThrIleIleSerGlyLeuGly-----IlePro	87
Qy	298	ATAATAGTGTCTATATATATCTTTTGGTACCTCAATCACTGCTTTTGGCCCGCGGA	357
Db	88	ValLeuGlyGluValPheSerIleLeuGlySerLeuIleGlyLeuLeuTyrProSerAsn	107
Qy	358	GAACAGACAAAACAGTAGTAGACAAATTTATTAATAGGGGAGAAATTTTGTGTGATACA	417
Db	108	AsnGluAsn-----ValTyrGlnIlePheMetAsnArgValGluGluLeuIleaspGln	125
Qy	418	CCGTTAACAGAAAGCAATAAAGCTAAAGTTTACAACTTTAGAGAGGATTTAGACAAATA	477
Db	126	LysIleLeuAspSerValArgSerArgAlaIleAlaAspLeuAlaAsnSerArgIleAla	145
Qy	478	TTACAAAGCTATAATACAGCATAGATGATGGAGAAAATTTAAAGACTACAGCTCCT	537
Db	146	ValGluTyrTyrGlnAsnAlaLeuGluLeuAspTyrArgLys-----	158
Qy	538	GGATTACCAACATCATCAGCATTAACAACAGCTGCTTGTACTCTTTAAATACGATTTGAG	597
Db	159	-----AsnProHisSerThr-----ArgSerAlaAlaLeuValLysGluArgPheGly	174
Qy	598	AATGTTCAATAGATTTTATTCGAGAAATACCTGCTTTCCAACTTTGAAACTTTATAAACG	657
Db	175	AsnAlaGluAlaIleLeuArgThrAsnMetGlySerPheSerGlnThrAsnTyrGluThr	194
Qy	658	CTATTACTACTATTATTCGCAAGCTGCTAATTTTCAATTTTAAATTTATTACACAAAGT	717
Db	195	ProLeuLeuProThrTyrAlaGlnAlaAlaSerLeuIleAlaLeuValMetArgAspVal	214
Qy	718	GCTGAATTTGGCTGATGGAATGCAGATATACATCTTCCAAATTTGAACTTAATGCT	777
Db	215	GlnIleTyrGlyLeuGluTyrPgl-----TyrProGln-----	225
Qy	778	GGAACTCAGATGACTATTATTAATCTTTTAAAGAAATATATACCTTAAATATAGTAACAT	837
Db	226	AsnAspIleAspLeuPheTyrLysGluGlnValSerTyrThrAlaArgTyrSerAspHis	245
Qy	838	TGTGCAATACCTATAGAGAGAGCTAATAAATCTTCGAAACGAACCTTAATATGATGG	897
Db	246	CysValGlnTyrTyrAsnAlaGlyLeuAsnLysLeuArgGlyThrGlyAlaLysGlnTyr	265
Qy	898	AGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATCGCTCAA	957

Db	266	ValAspTyrAsnArgPheArgArgGluMetAsnValMetValLeuAspLeuValAlaLeu	285
Qy	958	TTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTA	1017
Db	286	PheProAsnTyrAsp-----AlaArgIleTyrProLeuGln	297
Qy	1018	ACT-----GAACCTTACAGAGAAATTTATACAACTGAAATATAAATTTTGACCGCTCTACT	1071
Db	298	ThrAsnAlaGluLeuThrArgGluIlePheThrAspProValGly-----Ser	313
Qy	1072	TACCTTGAATTTCAACCCAATCTCGCTATATATGAATATATTTTAAACGCTTCAGGCTT	1131
Db	314	TyrValThrGlyGlnSerSerThrLeuIleSerTyrAspMetIleProAlaAlaLeu	333
Qy	1132	AGATTATTTTCAATTTTAGATGAATATATA-----TTTATACAAAAATGAA	1179
Db	334	ProSerPheSerThrLeuGluAsnLeuArgLysProAspPhePheThrLeuGln	353
Qy	1180	ACGTACGGGAATCGTTTGTATTGCGAATCGTAATAGTACTTACTTATGTACGACA	1239
Db	354	GluIle-----ArgMetTyrThrSerPheArgGlnAsn	364
Qy	1240	GGAACTGAAATTTATATATGAGAAAGAACAGGTCCACCACACAAAAAATTTTAATA---	1296
Db	365	GlyThrIleGluTyrTyrAsnTyrTyrGlyGlnArgLeuThrLeuSerTyrIleTyr	384
Qy	1297	-----CCATTGGAATCTTATAAATTTCAATTTGTAAGTATGATAGCAAGTAACCTCTACT	1350
Db	385	GlySerSerPheAsnLysTyrSerGlyValLeuAlaGlyAlaGluAspIleProVal	404
Qy	1351	TCCCT-----TTTCTTAAACATATAC	1371
Db	405	GlyGlnAsnAspIleTyrArgValValTyrThrTyrIleGlyArgTyrThrAsnSerLeu	424
Qy	1372	TTTCAATTAATCAATTTGAATTTTATTAATTAATTAATCACTAGCTAATAAATTAACATAT	1431
Db	425	LeuGlyValAsnProValThrPheTyrPheSerAsn-----AsnThrGlnLysThrTyr	442
Qy	1432	TCAGCTGGGGGAATTTATCTAATGNTAATAAACAACACTGATTTTCAATTTCTCTGTA	1491
Db	443	SerLysProLysGlnPheAlaGlyGlyIleLysThrIleAspSerGlyGluLeuThr	462
Qy	1492	AAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAGCTATAATAGTTATAGTCA	1551
Db	463	TyrGlu-----AsnTyrGlnSerTyrSerHis	471
Qy	1552	ATTTTATCCCAAGTTTCTTTTATTTAATTTATTTCTTATAAATTTGGATTAGCGCTAATA	1611
Db	472	ArgValSerTyrIleThrSerPheGluIleLysSerThrGlyGlyThrValLeuGlyVal	491
Qy	1612	TTATATACAGGTGATTTAGGATGACACACAGTAGTGTGTATAGAAATATGCAATATCA	1671
Db	492	Val-----ProIlePheGlyTyrThrHisSerSerAlaSerArgAsnAsnPheIleTyr	509
Qy	1672	GATAAATAATTTACATGATCCCAACATCAAGTAAACAGTCTTGTATACAACTCTAAG	1731
Db	510	AlaThrLysIleSerGlnIleProLeuAsnLysAlaSerArg-----ThrSerGlyGly	527
Qy	1732	GTAATTT-----GAAGGAGCTGCTGATCAGAGGAGAACTTGGTTTATTACAA	1779
Db	528	AlaValTyrAsnPheGlnGluGlyLeu-----TyrAsnGlyGlyProValMetLysLeuSer	546
Qy	1780	AGTCAGGG-----CGTTTAGAATTTACATGATAGAACCTCTTAATTTCTACAA	1827
Db	547	GlySerGlySerGlnValIleAsnLeuArgValAlaThrAspAlaLysGlyAlaSerGln	566
Qy	1828	TCATTATACATTAGACTTTCGATACGATCAAAATGTGTCTGGAAT---ACTCTCTCTAAT	1884
Db	567	ArgTyrArgIleArgGlyLeuArgTyrAlaSerAspArgAlaGlyLysPheThrIleSerSer	586
Qy	1885	ATATCTCTTACATACACAGGAGTAAATAGGAATACCACTCAACGACTCAAC-----AAC	1938







A:Reference number: 139813; MUID:93259939; PMID:8491716

A:Accession: 139813

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 9-58 <RE2>

A:Cross-references: UNIPARC:UPI00000B007B; GB:L03393; NID:g304150; PIDN:AAA22350.1; PID:

C:Genetics:

A:Gene: cryIIIA

C:Superfamily: Paraspinal crystal protein

C:Keywords: delta-endotoxin

Alignment Scores:

Pred. No.:	1.16e-32	Length:	652
Score:	616.50	Matches:	197
Percent Similarity:	41.71%	Conservative:	110
Best Local Similarity:	26.77%	Mismatches:	302
Query Match:	15.65%	Indels:	127
DB:	2	Gaps:	28

US-10-782-570-1 (1-2235) x A27323 (1-652)

Qy	1	GTGAATCAAAATAATAAATAATGAATATAGATTATC---GATTCAAGAATTTATCTTAT	57
Db	9	MetAenProAenAenArgSerGluHisAspThrIleLysThrThrGluAenAenGluVal	28
Qy	58	CTTCTTAACAGAAATATTGATCAATCTAGATACCTTACACAAATAATCCAAATCAACCA	117
Db	29	ProThrAen-----HisValGlnTyrProLeuAlaGluThrProAenProThr	44
Qy	118	TTACAAACACAAATACAAAGAGTGGCTCAATATGTCAAGGGAATACACAATATGGT	177
Db	45	LeuGluAenLeuAenTyrLysGluPheLeuArgMetThrAlaAenAen-----	60
Qy	178	GATAATTCGAGACATTTGCTAGTCTGATCAATTTGCTGCGTAGTGCAGGTACTATT	237
Db	61	---AenThrGluAlaLeuAenSerSerThrThrLysAspValIleGlnLysGlyIleSer	79
Qy	238	GTATCCGGTACTCTGTAGCCGGTATAGTGGCTCACTTCTATATCCGACCCGATAGGA	297
Db	80	ValValGlyAspLeuLeuGlyValValGly-----PheProPheGly	93
Qy	298	ATAATAGTGTCTATAATAATATCTTTGGTACCCTTAATCACTGTCTTTGGCCCGCGGA	357
Db	94	-----GlyAlaLeuValSerPheTyrThrAenPheLeuAenThrIleTyrProSerGlu	111
Qy	358	GAACAAGACAAACAGTAGTAGACAAATTTATTTAAATGGGAGAAATTTTGTGTATACA	417
Db	112	AspPro-----TrpLysAlaPheMetGluGlnValGluAlaLeuMetAspGln	127
Qy	418	CCGTTACAGAAAGCATAAACAGCTAAAGTTACAACTTTAGAGGATTTAGACAAATA	477
Db	128	LysIleAlaAspTyrAlaLysAenLysAlaLeuAlaGluLeuGlnGlyLeuGlnAenAen	147
Qy	478	TTACAAAGCTATAATACAGCATATAGATGATGGAGAAATTTAAAGACTACAAGCTCCT	537
Db	148	ValGluAenTyrValSerAlaLeuSerSerThrGlnLys-----	160
Qy	538	GGATTACCAATCATACAGCATTAACAACAGCTGCTTGTGATCTTTAAATACGATTGAG	597
Db	161	---AenProValSerSerArgAenProHisSerGlnGlyArgIleArgGluLeuPheSer	179
Qy	598	AATGTTCAATGATTTTATTCGAGAAATACCTGTTTCCAACTTGAACCTTATAAAGC	657
Db	180	GlnAlaGluSerHisPheArgAenSerMetProSerPheAlaIleSerGlyTyrGluVal	199
Qy	658	CTATTACTACTCTATTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTAACAACAGGT	717
Db	200	LeuPheLeuThrThrTyrAlaGlnAlaAlaAenThrHisLeuPheLeuLeuLysAspAla	219
Qy	718	GCTGAATTTGGCTGATGATGG-----AATGCAGATATACATCTTTCACAAATGAA	768
Db	220	GlnIleTyrGlyGluGluTyrGlyTyrGluLysGluAenPheIle-----	233

Qy	769	CCTAATGCTGGAACATCAGATGACTATTATATAAACTTTTAAAGAAATATATACCTAAATAT	828
Db	234	-----AlaGluPheTyrLysArgGlnLeuLysLeuThrGlnGluTyr	247
Qy	829	AGTAACATATTGTGCAATACCTATAGAGAAAGGACTAAATAAATTCGAAACGAACCTAAT	888
Db	248	ThrAspHisCysValLysTyrTyrAenValGlyLeuAspLysLeuArgGlySerTyr	267
Qy	889	ATGAGATGGAGTATATTATATGATATCGAAGATATATGACTATTACTGTATTAGTACT	948
Db	268	GluSerTrpValAenPheAenArgTyrArgGluMetThrLeuThrValLeuAspLeu	287
Qy	949	ATCGCTCAATTTCTTTTATATATAAAGAGATACAAAGATTCATAGGAGAAATAGGT	1008
Db	288	IleAlaLeuPheProLeuTyrAspValArgLeuTyrProLysGlu-----	302
Qy	1009	GGCATTTAAACTGAACCTTACAGAGAAATTTATACAACTGAAATATAATTTTGACCGTCTT	1068
Db	303	---ValLysThrGluLeuThrArgAspValLeuThrAspProIle-----	316
Qy	1069	ACTTACCTCGAAATTCACCCCAATCTCGCTATATATGAATATATATTTAACAGTTCAGGG	1128
Db	317	-----ValGlyValAen---AsnLeuArgGlyTyrGlyThrThrPheSerAen	331
Qy	1129	CTT-----AGATTATTTTCAATTTTAGATGAACCTTATATTTAT	1167
Db	332	IleGluAenTyrIleArgLysProHisLeuPheAspTyrLeuHisArgIleGlnPheHis	351
Qy	1168	ACAAAATGAAACG-----TAGGGAATCGTTTACTTGGTATTCGGAATTCGTAATAGA	1221
Db	352	ThrArgPheGlnProGlyTyrTyrGlyAsnAspSerPheAenTyrTyrSerGlyAenTyr	371
Qy	1222	---TCTACTTATGCTACGACAGGA-----ACTGAAATATATATATGAGAA	1263
Db	372	ValSerThrArgProSerIleGlySerAsnAspIleIleThrSerProPheTyrGlyAen	391
Qy	1264	AGAACAGTCCACCAACACAAACCTTTAATACCATTTGAATCC---TATAAAGTTTCA	1320
Db	392	LysSerSerGluProValGlnAenLeuGluPheAenGlyGluLysValTyrArgAlaVal	411
Qy	1321	ATTGTAACTAGACAGTAAGTAACTCTTACTTCCCTTTTCTTAACTATATCTTTTACAAT	1380
Db	412	AlaAenThrAenLeuAlaValTyrProSerAla-----ValTyrSerGlyVal	427
Qy	1381	AATCAAAATGAACTTTATTTAAATAATTCACCTAGTAAATAATTA-----ACATAT	1431
Db	428	ThrLysValGlnPheSerGlnTyrAsnAspGlnThrAspGluAlaSerThrGlnThrTyr	447
Qy	1432	TCAGCTGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCTCTGTAATA	1491
Db	448	AspSerLysArgAenValGlyAlaValSerTrpAspSerIleAspGlnLeuProGlu	467
Qy	1492	AAAGACTGTAACCAATTTATTAATTCCAAATTTGTTTACCAAGCTATAATAGTTAGTCAAT	1551
Db	468	ThrThrAspGluProLeuGluLys-----	475
Qy	1552	ATTTTATCCCAAGTTTCTTTATTTAATTTTCTTATAAATTTGATTTAGCGCTAAATATA	1611
Db	476	-----GlyTyrSerHisGlnLeuAenTyrValMetCysPhe	487
Qy	1612	TTATATACAGTGCATTTAGGA-----TGGACACACAGTAGTGTAAAT	1653
Db	488	LeuMetGlnGlySerArgGlyThrIleProValLeuThrThrThrHisLysSerValAsp	507
Qy	1654	AGAAATATGCAATATATCAGATAAAATAATTAATGATCCCAAGCAATCAAGGTAAACAGT	1713
Db	508	PhePheAenMetIleAspSerLysLysIleThrGlnLeuProLeuValLysAlaTyrLys	527
Qy	1714	CTTGATCAAACTCTAGGTAATTTGAAGGACCTGGTCAATACAGGAGAACTTGGTTTAT	1773
Db	528	LeuGlnSerGlyAlaSerValValAlaGlyProArgPheThrGlyGlyAspIleIleGln	547
Qy	1774	TTACAAAGTCAAGGGCGTTTATAGATTTACATGTAGAACTCTCT-----AATTTCTACACA	1827

Db 548 CysThrGluAsnGlySerAlaAlaThrIleTyrValThrProAspValSerTyrSerGln 567  
 QY 1828 TCTATTACATAGACTTCGATACCTACAAATGGTGTGGAAATCTCTTCCATAATATA 1887  
 Db 568 LysTyrArgAlaArgIleHisTyrAlaSerThrSer-----GlnIle 581  
 QY 1888 TCTCTTCAATACACGAGTAGTATAGAAATACCACTCAACGACTCAACACACACTTTTCT 1947  
 Db 582 ThrPheThrLeu---SerLeuAspGlyAlaPro-----PheAsnGlnTyrTyrPhe 597  
 QY 1948 GGTCAAAATATAAT-----AATTACATACGAGAGATTTTGGGTATTTCCAAATTT 1998  
 Db 598 AspLysThrIleAsnLysGlyAspThrLeuThrTyrAsnSerPheAsnLeuAlaSerPhe 617  
 QY 1999 CCAAGTACAGTAACATTAATCTTAATCGAAACATACCATTTATATTAATTCGTGCAGAT 2058  
 Db 618 SerThrProPheGluLeuSerGlyAsn---AsnLeuGlnIleGlyValThrGlyLeuSer 636  
 QY 2059 GTATCAAAATTCAAATTAATCAATTCATAAAATTTGAATTTATACCAATTT 2106  
 Db 637 AlaGlyAspLysVal---TyrIleAspLysIleGluPheIleProVal 651

RESULT 11  
 S00873  
 parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
 N:Alternate names: parasporal crystal protein cryA4  
 C:Species: Bacillus thuringiensis subsp. thuringiensis  
 C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Oct-2004  
 C:Accession: S00873  
 R:Brizzard, B.L.; Whiteley, H.R.  
 Nucleic Acids Res. 16, 2723-2724, 1988  
 A>Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
 A:Reference number: S00873; PMID:86203216; PMID:3362680  
 A:Accession: S00873  
 A:Molecule type: DNA  
 A:Residues: 1-1228 <BRI>  
 A:Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:g40264; PIDN  
 C:Genetics:  
 A:Gene: cryA4  
 A:Start codon: TTG  
 C:Superfamily: Parasporal crystal protein  
 C:Keywords: delta-endotoxin

Alignment Scores:  
 Pred. No.: 4,876-32 Length: 1228  
 Score: 607.00 Matches: 209  
 Percent Similarity: 40.32% Conservative: 114  
 Best Local Similarity: 26.09% Mismatches: 294  
 Query Match: 15.41% Indels: 184  
 DB: 2 Gaps: 35

US-10-782-570-1 (1-2235) x S00873 (1-1228)

QY 1 GTGAATCAAAATAAATAATGAATATGATGATTCGATTCAAGAAATTTATCTATCT 60  
 Db 1 MetThrSerAsnArgLysAsnGluAsnGluIleIleAsnAla-----Val 15  
 QY 61 TCTAACAGAAATATTGATCATCTTAGATACCCCTTACACAAATAATCCAAATCAACCAATTA 120  
 Db 16 SerAsnHisSerAlaGlnMetAspLeuLeuPro----- 26  
 QY 121 CAAACACAAATTAACAGAGTGGCTCAATATGTGTCAAGGAAATACACAAATATGATGAT 180  
 Db 27 ---AspAlaArgIleGluAspSerLeuCysIleAlaGluGlyAsn----- 40  
 QY 181 AATTTCGAGACATTTGCTAGTCTGATACAAATTCGTGACGTAGTGCAGGTACTATTGTA 240  
 Db 41 AsnIleAspProPheValSerAlaSerThr-----ValGlnThrGlyIleAsnIle 57  
 QY 241 TCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGCATAGGAATA 300  
 Db 58 AlaGlyArgIleLeuGlyValLeuLeuGly-----ValProPhe 69

QY 301 ATAGGTGCTATAATAATATCTTTTGGTACCTAATCACTGCTCTTTTGGCCCGCGAGAA 360  
 Db 70 AlaGlyGlnLeuAlaSerPheTyrSerPheLeuValGlyGluLeuTyrProArgGlyArg 89  
 QY 361 CAAGACAAAACAGATATGACACAAATTTATTAAATGGGAGAAATTTTGTGTATACACCG 420  
 Db 90 AspGln-----TrpGluIlePheLeuGluHisValGluGlnLeuIleAsnGlnGln 106  
 QY 421 TTAACAGAAAGCATAAACACAGCTAAAGCTTACAACTTTAGAGAGATTTAGACAAATATA 480  
 Db 107 IleThrGluAsnAlaArgAsnThrAlaLeuAlaArgLeuGlnGlyLeuGlyAspSerPhe 126  
 QY 481 CAAAGCTTATAATACAGCATTAGATGATTGGAGAAATTTAAAGACACTACAGCTCCTCGA 540  
 Db 127 ArgAlaTyrGlnGlnSerLeuGluAspTrpLeuGlu-----AsnArgAspAsp 142  
 QY 541 TTACCACCATCATCAGCATTAACAACAGCTGCCTTGACTCTTAAATACGATTTTGAGAAT 600  
 Db 143 AlaArgThrArgSerValLeuTyrThrGlnTyrIleAlaLeuGluLeu----- 158  
 QY 601 GTTCACAAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAACGCTA 660  
 Db 159 -----AspPheLeuAsnAlaMetProLeuPheAlaIleArgAsnGlnGluValPro 175  
 QY 661 TTACTACTCTATTATGCGCAAGCTGCTAAATTTTTCATTTTAAATTTTATCAACAAGGTGCT 720  
 Db 176 LeuLeuMetValTyrAlaGlnAlaAlaAsnLeuHisLeuLeuLeuLeuArgAspAlaSer 195  
 QY 721 GAATTTGGCTGATGAATGGAATGCAGATATACATCTCTTCACAAAATTTGAACCTTAATGCTGGA 780  
 Db 196 LeuPheGlySerGluPheGlyLeu----- 203  
 QY 781 ACATCAGATGAC-----TATTATAAACTTTTAAAGAAATATACCTTAATATAGT 831  
 Db 204 ThrSerGlnGluIleGlnArgTyrGluArgGlnValGluArgThrArgAspTyrSer 223  
 QY 832 AACTATTGTGCAAAATCACTATAGAGAGAGACTTAAATAAACTTCCGAAACGAACCTAATATG 891  
 Db 224 AspTyrCysValGluTyrPyrAsnThrGlyLeuAsnSerLeuArgGlyThrAsnAlaAla 243  
 QY 892 AGATGGAGTATATTAAATGATTTATCGAAGATATATGACTATTACTGTATTAGATATATC 951  
 Db 244 SerTrpValArgTyrAsnGlnPheArgArgAspLeuThrLeuGlyValLeuAspLeuVal 263  
 QY 952 GCTCAATTTTCTTTTATGATATAAGAGATACAAAGATTCATCAATAGGAGAAATAGGTGCG 1011  
 Db 264 AlaLeuPheProSerTyrAspThrArgThrTyrProIleAsn----- 277  
 QY 1012 ATTAAACTGAACCTTCAAGAGAAATTTATACA-----ACTGAATAAAT 1056  
 Db 278 ThrSerAlaGlnLeuThrArgGluValTyrThrAspAlaIleGlyAlaThrGlyValAsn 297  
 QY 1057 TTTGACCGCTCTTACT---TACCTTTGAAATTCACCCCAATCTCGCTATAATGGAATATAAT 1113  
 Db 298 MetAlaSerMetAsnTrpTyrAsnAsnAsnAlaProSerPheSerAlaIleGluAlaAla 317  
 QY 1114 TTAACAGCTTCAGGCTTAGATTTATTTTCATTTTGTAGTGAACCTT---ATATTT----- 1164  
 Db 318 AlaIleArgSerPro---HisLeuLeuAspPheLeuGluGlnLeuThrIlePheSerAla 336  
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 Db 337 SerSerArgTyrPyrAsnThrArgHisMetThrTyrTrpArgGlyHisThrIleGlnSer 356  
 QY 1192 CGTTTAGTTGTGATTTGCGAATCGTAATAGATCTACTTATGTACGACAGCAAGCAATGAAAT 1251  
 Db 357 ArgProIleGly---GlyGlyLeuAsnThrSerThrHisGlyAlaThrAsnThrSerIle 375  
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 Db 376 -----AsnProValThrLeuArgPheAlaSerArgAspValTyrArg 389

QY 1300 TTTGAATCTATAAAGTTTCAATGTAAGTATGATAGACAGTAACCTCTACTTCCCTTTT 1359  
 Db 390 ThrGluSerTyrAlaGlyValLeuLeuTrpGlyIleTyrLeuGluProIleHiglyVal 409  
 QY 1360 CCTACATATCTTTTACAAATTAATCAAATTTGAACCTTTATTTAAATAATTTACCTAGTAAT 1419  
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 QY 1420 AAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAATAAACAACATGATTTTCAA 1479  
 Db 422 -----11eSerAspArgGlyThrAlaAsnTyrSer 431  
 QY 1480 TTTCTGTGTAATA-----AAAGACTGTAAACCAATTTAATCCCAAT 1521  
 Db 432 GlnProTyrGluSerProGlyLeuGlnLeuIleAspSerGluThrGluLeuProProGlu 451  
 QY 1522 TGTTTA-----CCAAGCTATAATATGATGATATTTATTTATCCAGTTTCTTTTATTT 1575  
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 QY 1576 AATTAATCTATAAATTTGGATTAGCGCTAATAATA-----TTATATACAGGTGCATTAGGA 1632  
 Db 472 LeuGlnSer-----ArgValAsnValProValTyrSer----- 482  
 QY 1633 TGGACACAGTAGTGTAAATAGAAATATGCAATATCAGATAAATAATTAATACATGATC 1692  
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 QY 1693 CCAGCAATCAAGAGTAAACAGTCTGATACAAACTCTAAGGTAATTTGAAGGACCTGGTCAT 1752  
 Db 503 ProMetValIleAlaSerGluLeuProGlnGlyThrThrValValArgGlyProGlyPhe 522  
 QY 1753 ACAGAGAGAACTTGGTTTATTTTCAAAAGTCAA-----GGCGCTTTAGAGATACA 1803  
 Db 523 ThrGlyGlyAspIleLeuArgArgThrAsnThrGlyGlyPheGlyProIleArgValThr 542  
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 Db 543 ValAsnGlyPro-----LeuThrGlnArgTyrArgIleGlyPheArgTyrAlaSerThrVal 561  
 QY 1858 -----AATGGTCTCGAAATCTCTCTCTAATATATCTCTTACAAATA 1899  
 Db 562 AspPheAspPhePheValSerArgGlyGlyThrThrValAsnAsnPheArgPhe----- 579  
 QY 1900 CCAGAGTAATAGGAATACCACCTCAACGACTCAACAAACACTTTTCTGGTACAAATAT 1959  
 Db 580 -----LeuArgThrMetAsnSerGly----- 586  
 QY 1960 AATAATTTTACATACGAGATTTTGGGTATTTCCCAATTTCCCAAGTACAGTAACATTACCT 2019  
 Db 587 AspGluLeuIleTyrGlyAsnPheValArgArgAlaPheThrThr----- 601  
 QY 2020 TTAATCGAAACATACCATTTTATATTTAATCGT---GCAGATGTA----- 2061  
 Db 602 -----ProPheThrPheThrGlnIleGlnAspIleIleArgThrSerIle 616  
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 QY 2170 ACATTTTTCACAAATCATACAAAAATACTTTAATATAGAGGCCACAAACTATGATATT 2229  
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I39815  
 insecticidal protein cryV - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Oct-2004  
 C:Accession: I39815  
 R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59, 1683-1687, 1993  
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
 iensis subsp. kurstaki.  
 A:Reference number: I39815; MUID:93298009; PMID:8517758  
 A:Accession: I39815  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
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 A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI0000036008; GB:M98544; NID:G142767; PIDN:  
 C:Genetics:  
 A:Gene: cryV  
 C:Superfamily: Parasporal crystal protein  
 Alignment Scores:  
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 QY 100 AATAATCCAATCAACATTACAAATTTACAAAGAGTGGCTCAATATATGTCAA 159  
 Db 28 AsnGluThrAspIleGluLeuGlnAsnIleAsnHisGluAspCysLeuLysMet----- 45  
 QY 160 GGGNATACAAATATGATGATATTTTCGACACATTTCTAGTCTGATACAAATTTGCTGCA 219  
 Db 46 -----SerGluTyr---GluAsnValGluProPheValSerAlaSerThrIleGln--- 61  
 QY 220 GTTAGTCAGGTACTATTGTATCGGTACTCTGTAGCCGTATAGTGGCTCCTTCT 279  
 Db 62 -----ThrGlyIleGlyIleAlaGlyLys 69  
 QY 280 ATATCCGCGCCGATAGGAATA-----ATAGGTGCTATAATAATATCTTTTGGTACCCTA 333  
 Db 70 IleLeuGlyThrLeuGlyValProPheAlaGlyGlnValAlaSerLeuTyrSerPheIle 89  
 QY 334 ATCATCTCTTTTGGCCCGGGAGAACAGACAAACAGTATGGACACAAATTTATATAA 393  
 Db 90 LeuGlyLeuLeuTrpProLysGly-----LysAsnGlnTrpGluIlePheMetGlu 106  
 QY 394 ATGGGAGAAATTTTGTGTATACACCCGTTAAACAGAAAGCATAAACAGCTAAAGTTACAA 453  
 Db 107 HisValGluGluIleIleAsnGlnLysIleSerThrTyrAlaArgAsnLysAlaLeuThr 126  
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 QY 565 CAAGCTCCCTTGACTCTTAAATACGATTTGAGAAATGTTTCAATGATTTTATTCGAGAA 624  
 Db 160 SerGlnTyrIleAlaLeuGluLeuMet-----PheValGlnLys 172  
 QY 625 ATACCTGTTTCCAACTTGAACCTTATPAAACGCTATTACTATTATTCGCAAGCT 684  
 Db 173 LeuProSerPheAlaValSerGlyGluGluValProLeuLeuProIleTyrAlaGlnAla 192







Db 614 ---LeuAspValGlnSerThrPheThrIleGlyAlaTrpAsnPheSerSerGlyAsnGlu 632  
Qy 2080 -----ATTGATAAAATGAATTTATATACCAATTAATCTCTGTAGCGCAAAATAGAGAA 2133  
Db 633 ValTyrIleAspArgIleGluPheValProValGluValThrTyrGluAlaGluTyrAsp 652  
Qy 2134 AAACAAAATAGAACTATCCAAACAAAATAAATACATTTTTCACAAATCATACAAA 2193  
Db 653 -----PheGluLeuAlaGlnGluValThrAlaLeuPheThrSerThrAsnPro 669  
Qy 2194 AATCTTTAATATAGAGCCACAAACTATGATTTGAT 2232  
Db 670 ArgGlyLeuLeuThrAspValIleAspTyrHisIleAsp 682

RESULT 14

825383  
N:Alteparal crystal protein cryIIal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 05-Oct-2004  
C:Accession: S25383  
R:Fallor, R.; Rippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
A:Reference number: S25383; MUID:92269582; PMID:1588820  
A:Accession: S25383  
A:Molecule type: DNA  
A:Residues: 1-719 <TAI>  
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI000002DB73; EMBL:X62821; NID:940289; PIDN  
C:Genetics:  
A:Gene: cryV  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin

Alignment Scores:  
Pred. No.: 1.22e-30 Length: 719  
Score: 585.50 Matches: 207  
Percent Similarity: 40.10% Conservative: 111  
Best Local Similarity: 26.10% Mismatches: 294  
Query Match: 14.86% Indels: 181  
DB: 2 Gaps: 34

US-10-782-570-1 (1-2235) x S25383 (1-719)

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Db 8 LysHisGlnSerPheSerAsnAlaLysValAspLysIleSerThrAspSerLeuLys 27  
Qy 100 AATAATCCAAATCAACCACTTACAAACACAAATTAACAAGAGTGCTCAATATGTGCAA 159  
Db 28 AsnGluThrAspIleGluLeuGlnAsnIleAsnHisGluAspCysLeuLysMet----- 45  
Qy 160 GGGATAACAAATATGGTGATTAATTCGAGACATTTGCTAGTGTGATACAAATTCCTGCA 219  
Db 46 -----SerGluTyr---GluAsnValGluProPheValSerAlaSerThrIleGln--- 61  
Qy 220 GTTAGTCAGGTACTATTGTATCCGGTACTCTGTTAGCGGTATAGTGGGCTCACTTCT 279  
Db 62 -----ThrglyIleGlyLeuAlaGlyLys 69  
Qy 280 ATATCGGACCGATAGGAATA-----ATAGTGTCTAATAATAATATCTTTGGTACCTTA 333  
Db 70 IleLeuGlyThrLeuGlyValProPheAlaGlyGlnValAlaSerLeuTyrSerPheIle 89  
Qy 334 ATCACTGTCTTTTGGCCGCGGAGAACAAAGACAGATGATGAGACAAATTTTATTA 393  
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Qy 394 ATGGGAGAAATTTTGTGATACACCGTTAACAGAAAGCATTAACAGCTAAAGTTACAA 453  
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Db 160 SerGlnTyrIleAlaLeuGluLeuMet-----PheValGlnLys 172  
Qy 625 ATACCTGTTTCCAACTTGAACCTTTATAAACGCTTATTAACCTTATTAATTCGCAAGCT 684  
Db 173 LeuProSerPheAlaValSerGlyGluValProLeuLeuProIleTyrAlaGlnAla 192  
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Qy 805 TTAAAGAGAAATATACCTTAATATAGTAACCTTATGCAAAATACCTATATAGAGAGCTA 864  
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Db 284 Pro-----IleLysThrThrAlaGlnLeuThrArgGluVal 295  
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Qy 1273 CCACCCCAACAAAACCTTTAATACCATTTGAATCC-----TATAAAGTTTCAAT 1323  
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 Qy 1555 TATCCCAAGTTTCTTTTATTAATATTATTCCTATAAAATGGATTAGCCCTAAATATTA 1614  
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 Db 491 -----TyrThrHisArgSerAlaAspArgThrAsnThrIleGluPro 504  
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 Db 505 AsnSerIleThrGlnIleProLeuValIleAlaPheAsnLeuSerSerGlyAlaAlaVal 524  
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 N;Alternate names: parasporal crystal protein cryID  
 C;Species: Bacillus thuringiensis  
 C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 05-Oct-2004  
 C;Accession: S11446  
 R;Hoefte, H.; Soetaert, P.; Janssens, S.; Referoen, M.  
 Nucleic Acids Res. 18, 5545, 1990  
 A;Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific  
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 A;Status: preliminary  
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 A;Molecule type: DNA  
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A;Cross-references: UNIPROT:P19415; UNIPARC:UPI000002COA3; EMBL:X54160; NID:940279; PIDN  
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 C;Keywords: Delta-endotoxin  
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 Score: 576.00 Matches: 198  
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 Best Local Similarity: 26.54% Mismatches: 275  
 Query Match: 14.62% Indels: 154  
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 Db 4 AsnAsnGlnAsnGlnCysValProTyrAsn-----CysLeu 15  
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 Db 16 SerAsnProIysGluIleLeuGlyGlu-----GluArgLeuGluThrGlyAsnThr 33  
 Qy 211 ATTGCTCAGTTAGTCAGGTACTATT-----GTATCCGCTACTCTGTAGCCGGTATA 264  
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 Qy 505 GATTGGAGAAATTTAAAGACATACAGCTCTGGATTACCACCATCATCAGCATACAA 564  
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 Qy 685 GCTAATTTCTTAAATTTTATACAAAGGTCTCAATTTGGCTGATGAATGAATGCA 744  
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Db 371 LeuAspAsnSerAsnProValAlaGlyIle----- 380
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QY 1663 GCAATATCAGATAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1722
Db 454 GluValSerProSerArgIleThrGlnIleProTrpValValHisThrLeuAlaSer 473
QY 1723 AACTCTAAGGTAAATGAAGGACTGTGTCATACAGGAGAACTTGTTTATTTTACAAAGT 1782
Db 474 GlyAlaSerValIleLysGlyProGlyPheThrGlyGlyAspIleLeuThrArgAsnSer 493
QY 1783 CAAGGG-----CGTTTAGAGATTACATGTAGAACTCCTTAATTTCTACAA 1827
Db 494 MetGlyGluLeuGlyThrLeuArgValThrPheThrGlyArgLeuPro-----Gln 510
QY 1828 TCCTTATACATAGACTTCGATACGCTACA-----AATGGTCTGGA----- 1869
Db 511 SerTyrTyrIleArgPheArgTyrAlaSerValAlaAsnArgSerGlyThrPheArgTyr 530
QY 1870 AATFACTCTTCTAATATATCTCTTACAATACAGGAGTAAATAGGAATACCACCTCAACGA 1929
Db 531 SerGlnProProSerTyrGlyIleSerPheProLysThrMetAspAlaGlyGluProLeu 550
QY 1930 CTCACAAACACTTTTCTGGTCAAAATTAATAATTTACAATACGAGATTTTGGGTAT 1989
Db 551 ThrSerArgSerPheAlaHisThrThrThrPheThr----- 562
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QY 1990 TTCCAATTTCCAGTACAGTAAACATTACCTTTAAATCGAAACATACCACTTTATTTAAT 2049
Db 563 -----ProIleThrPheSer 567
QY 2050 CGTCAGATGTATCAAAATTCATTTTAATC-----ATTGATAAAATTGAA 2094
Db 568 ArgAlaGlnGluGluPheAspLeuTyrIleGlnSerGlyValTyrIleAspArgIleGlu 587
QY 2095 TTTATACCAATTTACTTCTCTGTAGCGCCAAATAGAGAAAAACAAAAATTAGAAACTATC 2154
Db 588 PheIleProValThrAlaThrPheGluAlaGluTyrAsp-----LeuGluArgAla 604
QY 2155 CAAACAAAAATAAATACATTTTTCACAAATCATACAAAAAATACCTTTAAATATAGAGCC 2214
Db 605 GlnLysValValAsnAlaLeuPheThrSerThrAsnGlnLeuGlyLeuLysThrAspVal 624
QY 2215 ACAAACTATGATTTGAT 2232
Db 625 ThrAspTyrHisIleAsp 630
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Search completed: January 12, 2006, 06:42:48  
Job time : 86.5 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 12, 2006, 06:15:49 ; Search time 241.5 Seconds  
(without alignments)

13058.847 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaactcaaaataataa.....caaaactgatattgattaa 2235

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2\_1/USPTO\_spool\_p/US10782570/runat\_12012006\_060221\_7515/app.query.fasta\_1.2375  
-DB=Uniprot -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptp -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10782570@cgm\_1\_1\_418@runat\_12012006\_060221\_7515 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRA=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1158	29.4	1180	CR4AA_BACTI	P16480 bacillus th
2	1158	29.4	1180	Q7AL67_BACTI	Q7al67 bacillus th
3	906.5	23.0	1128	Q9FDC0_BACTF	Q9fdc0 bacillus th
4	901	22.9	1109	C28AA_BACTF	Q9x682 bacillus th
5	897	22.8	675	C10AA_BACTI	P09662 bacillus th
6	897	22.8	675	Q8KNV2_BACTI	Q8knv2 bacillus th
7	842.5	21.4	650	Q8VNX2_BACTV	P05519 bacillus th
8	819	20.8	1136	CR4BA_BACTI	Q7al72 bacillus th
9	819	20.8	1136	Q7AL72_BACTI	Q7al72 bacillus th
10	801.5	20.3	688	Q8VNX1_BACTV	Q8vnx1 bacillus th
11	796	20.2	683	Q75VA2_BACTE	Q75va2 bacillus th
12	787.5	20.0	1169	CR8BA_BACTE	Q45705 bacillus th
13	755.5	19.2	688	Q5W7N9_BACTU	Q5w7n9 bacillus th
14	709	18.0	682	C19BA_BACTH	O86170 bacillus th
15	708.5	18.0	1169	Q56B08_BACTU	Q56b08 bacillus th
16	706	17.9	659	CR3BA_BACTO	P17969 bacillus th

17	699	17.7	829	2	Q6BE06_BACTU	Q6be06 bacillus th
18	691	17.5	652	1	CR3BB_BACTU	Q06117 bacillus th
19	689	17.5	648	1	C19AA_BACTU	Q32307 bacillus th
20	689	17.5	1138	1	CR7AB_BACTU	Q35708 bacillus th
21	688	17.5	1138	1	CR7AA_BACTU	Q3749 bacillus th
22	686.5	17.4	660	2	Q8RQU6_BACTA	Q8rqu6 bacillus th
23	686	17.4	825	2	Q6BE09_BACTU	Q6be09 bacillus th
24	682.5	17.3	1236	2	Q939T3_BACTU	Q939t3 bacillus th
25	680	17.3	1280	2	Q8VUK9_BACTU	Q8vuk9 bacillus th
26	677.5	17.2	1157	1	CR8AA_BACTU	Q45704 bacillus th
27	672	17.1	1160	1	CR8CA_BACTP	Q45706 bacillus th
28	672	17.1	1160	1	Q6RZK6_BACTU	Q6rzk6 bacillus th
29	661	16.8	1138	1	CR7AB_BACTU	Q45707 bacillus th
30	659.5	16.7	686	2	Q75QO5_BACTE	Q75qo5 bacillus th
31	655.5	16.6	1157	1	CR9CA_BACTO	Q45733 bacillus th
32	654.5	16.6	1163	2	Q5XLA8_BACTP	Q5xla8 bacillus th
33	652	16.6	1169	1	CR9DA_BACTP	Q6014 bacillus th
34	636.5	16.2	1144	2	Q8KZL7_BACTG	Q8kzl7 bacillus th
35	635	16.1	1154	2	Q6QAN9_BACTG	Q6qan9 bacillus th
36	631	16.0	1254	2	Q8VUL0_BACTU	Q8vul0 bacillus th
37	630	16.0	826	1	C27AA_BACTH	Q9e597 bacillus th
38	625	15.9	1150	1	CR9EA_BACTA	Q9zn19 bacillus th
39	625	15.9	1150	2	Q71RE4_BACTU	Q71rp4 bacillus th
40	623.5	15.8	1231	2	Q8KNY2_BACTU	Q8kny2 bacillus th
41	620	15.7	1340	2	Q589X2_PAEPP	Q589x2 paenibacill
42	620	15.7	1344	2	Q765X7_9BACL	Q765x7 paenibacill
43	616.5	15.7	644	1	CR3AA_BACTD	P0a381 bacillus th
44	616.5	15.7	644	1	CR3AA_BACTM	P0a380 bacillus th
45	616.5	15.7	644	1	CR3AA_BACTT	P0a379 bacillus th

#### ALIGNMENTS

RESULT 1

CR4AA\_BACTI ID CR4AA\_BACTI STANDARD; PRT; 1180 AA.  
AC P16480;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Pesticidal crystal protein cry4Aa (insecticidal delta-endotoxin  
DE CryIVA(a)) (crystalline entomocidal protoxin) (135 kDa crystal  
DE protein).  
GN Name=cry4Aa; Synonyms=cryIVA(a), isxH4;  
OS Bacillus thuringiensis subsp. israelensis.  
OG Plasmid 72 Kb.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1430;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sen K., Honda G., Koyama N., Nishida M., Neki A., Sakai H., Himeno M.,  
RA Komano T.;  
RT "Cloning and nucleotide sequences of the two 130 kDa insecticidal  
RT protein genes of Bacillus thuringiensis var. israelensis.";  
RL Agric. Biol. Chem. 52:873-878(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=88015571; PubMed=2821500;  
RA Ward E.S., Ellar D.J.;  
RT "Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene  
RT encoding a 130 kDa delta-endotoxin.";  
RL Nucleic Acids Res. 15:7195-7195(1987).  
RN [3]  
RP MUTAGENESIS STUDIES.  
RX MEDLINE=94307434; PubMed=7913448; DOI=10.1016/0014-5793(94)00604-0;  
RA Nishimoto T., Yoshie H., Ihara K., Sakai H., Komano T.;  
RT "Functional analysis of block 5, one of the highly conserved amino  
RT acid sequences in the 130-kDa CryIVA protein produced by Bacillus  
RT thuringiensis subsp. israelensis.";  
RL FEBS Lett. 348:249-254(1994).  
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
CC epithelial cells of insects.

Db	131	SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr	150
Qy	487	TATAAATACAGCATTTAGATGATTCGAGAAAATTAATAAGACTACAAAGCTCTCGATTACCA	546
Db	151	TyrHisAsnHisLeuIlysthrTrpGlu-----AsnAsnProAsnProGln	165
Qy	547	CCATCATCAGCATTACACAACAGCTGCTTGACTCTTAAAAATACGATTTGAGAATGTTCCAC	606
Db	166	AsnThrGlnAspValArgThrGlnIleGlnLeuValHisThrHisPheGlnAsnValIle	185
Qy	607	AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACTTCGAAACTTATAAAACGCTA	660
Db	186	ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu	205
Qy	661	TTACTCTCTATTATTCGCAAGCTGCTAAATTTTCATTAAATTTATTACAAACAGGTGCT	720
Db	206	ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValIleAsnGlnAlaVal	225
Qy	721	GAATTCGGCTGATGAATGGAAATGCGATATACATCCTTCACAAATGGAACCTAATGCTGGA	780
Db	226	LysPheGluAlaTyrIleuLysAsnAsnArgGlnPheAspTyrIleuGluPro---LeuPro	244
Qy	781	ACATCAGATGACATTTATTAACCTTTTAAAGAAAATATATACCTTAATATAGTACTATTGT	840
Db	245	ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys	264
Qy	841	GCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACT-----	885
Db	265	ValThrTyrIlystysGlyLeuAsnLeuIleIlysthrThrProAspSerAsnLeuAsp	284
Qy	886	---AATATGAGATGGAGTATTAATATGATATTCGAGATATATGACTATTACTGTATTA	942
Db	285	GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu	304
Qy	943	GATACTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGATTCATAGGAAGA	1002
Db	305	AspLeuValAlaLeuPheProAsnTyrAspValGlyIlystyrProIle-----	320
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Db	321	-----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu	337
Qy	1063	CGTCTTACTTCTGAAATTCACCCCACTCTCGCTATTAATGGAATATATATTAACACCGT	1122
Db	338	GluSerProTyrIlystyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg	355
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Db	356	ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluIlysalGlnThr	374
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Db	375	ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn	393
Qy	1234	ACGACAGGAACCTGAAATTTATATATGAGAGAAACAGGCTCCACCACCAACAAAACCTTTA	1293
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Qy	1354	CTTTTTCCTTAACATATCTTTACAAATTAATCAAAATGAACTTTTAAATTAATTAATCCT	1413
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Qy	1414	-----AGTAATAAAATTAACATATCAATATTCAGCTGGGGGGAATTTATCTAATGATA	1464
Db	452	ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn	470
Qy	1465	ACAACCTGATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTAATTAATCCTAATGT	1524
Db	471	LysAsnIlePheGlyLeuProIleuLysTyrArgGluAsnGlnGlyAsnProThrLeu	490

Db	131	SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr	150
Qy	487	TATAAATACAGCATTTAGATGATCGAGAAAATTAATAAGACTACAAAGCTCTCGATTACCA	546
Db	151	TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln	165
Qy	547	CCATCATCAGCATTACACAACAGCTGCTTGACTCTTAAAAATACGATTTGAGAATGTTCCAC	606
Db	166	AsnThrGlnAspValArgThrGlnIleGlnLeuValHisThrHisPheGlnAsnValIle	185
Qy	607	AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACTTCGAACTTATAAAACGCTA	660
Db	186	ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu	205
Qy	661	TTACTCTCTATTATCGCAAGCTGCTAAATTTTCATTAAATTTATTACAAACAGGTGCT	720
Db	206	ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValIleAsnGlnAlaVal	225
Qy	721	GAATTCGGCTGATGAATGGAAATGCAGATATACATCTCTTCAAAATGAACCTAATGCTGGA	780
Db	226	LysPheGluAlaTyrIleLysAsnAsnArgGlnPheAspTyrIleuGluPro---LeuPro	244
Qy	781	ACATCAGATGACATTTATTAACCTTTTAAAGAAAATATATACCTTAATATAGTACTATTGT	840
Db	245	ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys	264
Qy	841	GCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACT-----	885
Db	265	ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp	284
Qy	886	---AATATGAGATGGAGTATTAATATGATATTCGAGATATATGACTATTACTGTATTA	942
Db	285	GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu	304
Qy	943	GATACTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGATTCATATAGGAAGA	1002
Db	305	AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle-----	320
Qy	1003	ATAGGTGGCATTAATAACTGAACTTACAAGAGAAATTTATACAACCTGAATAATTTTGAC	1062
Db	321	-----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu	337
Qy	1063	CGTCTTACTTCTGAAATTCACCCCACTCTCGCTATAATGGAATATATATTAACACCGT	1122
Db	338	GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg	355
Qy	1123	TCAGGGCTGAGATATTTTCATTTTAGATGAACCTTATATTTATACAAAATAATGAACG	1182
Db	356	ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr	374
Qy	1183	TACGGGAATCGTTAGTTGGTATTCGGAATCGTAATAGATCTACTTATGCT-----	1233
Db	375	ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn	393
Qy	1234	ACGACAGGAACCTGAAATTTATATATGAGAGAAACAGGCTCCACCACCAACAAAATTTTA	1293
Db	394	IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu	413
Qy	1294	ATACCAATTTGAATCCTATAAAGTTTCAATTTGTAATCTGATAGACAGTAACCTCTACTTC	1353
Db	414	-----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn	431
Qy	1354	CTTTTCCTTAACATATCTTTACAAATTAATCAAAATGAACCTTTTAAATTAATTAACCT	1413
Db	432	LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr	451
Qy	1414	-----AGTAATAAAATTAACATATCAATATCACTGGGGGGAATTTATCTAATGATAAAA	1464
Db	452	ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn	470
Qy	1465	ACAACCTGATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATTAATTAATCCTAAATGT	1524
Db	471	LysAsnIlePheGlyLeuProIleLysLysArgArgGluAsnGlnGlyAsnProThrLeu	490

Db	131	SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr	150
Qy	487	TATAAATACAGCATTTAGATGATCGAGAAAATTAATAAGACTACAAAGCTCTCGATTACCA	546
Db	151	TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln	165
Qy	547	CCATCATCAGCATTACACAACAGCTGCTTGACTCTTAAAAATACGATTTGAGAATGTTCCAC	606
Db	166	AsnThrGlnAspValArgThrGlnIleGlnLeuValHisThrHisPheGlnAsnValIle	185
Qy	607	AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACTTCGAACTTATAAAACGCTA	660
Db	186	ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu	205
Qy	661	TTACTCTCTATTATCGCAAGCTGCTAAATTTTCATTAAATTTATTACAAACAGGTGCT	720
Db	206	ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValIleAsnGlnAlaVal	225
Qy	721	GAATTCGGCTGATGAATGGAAATGCAGATATACATCTCTTCAAAATGAACCTAATGCTGGA	780
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Qy	781	ACATCAGATGACATTTATTAACCTTTTAAAGAAAATATATACCTTAATATAGTACTATTGT	840
Db	245	ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys	264
Qy	841	GCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACT-----	885
Db	265	ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp	284
Qy	886	---AATATGAGATGGAGTATTAATATGATATTCGAGATATATGACTATTACTGTATTA	942
Db	285	GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu	304
Qy	943	GATACTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGATTCATATAGGAAGA	1002
Db	305	AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle-----	320
Qy	1003	ATAGGTGGCATTAATAACTGAACTTACAAGAGAAATTTATACAACCTGAATAATTTTGAC	1062
Db	321	-----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu	337
Qy	1063	CGTCTTACTTCTGAAATTCACCCCACTCTCGCTATAATGGAATATATATTAACACCGT	1122
Db	338	GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg	355
Qy	1123	TCAGGGCTGAGATATTTTCATTTTAGATGAACCTTATATTTATACAAAATAATGAACG	1182
Db	356	ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr	374
Qy	1183	TACGGGAATCGTTAGTTGGTATTCGGAATCGTAATAGATCTACTTATGCT-----	1233
Db	375	ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn	393
Qy	1234	ACGACAGGAACCTGAAATTTATATATGAGAGAAACAGGCTCCACCACCAACAAAATTTTA	1293
Db	394	IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu	413
Qy	1294	ATACCAATTTGAATCCTATAAAGTTTCAATTTGTAATCTGATAGACAGTAACCTCTACTTC	1353
Db	414	-----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn	431
Qy	1354	CTTTTCCTTAACATATCTTTACAAATTAATCAAAATGAACCTTTTAAATTAATTAACCT	1413
Db	432	LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr	451
Qy	1414	-----AGTAATAAAATTAACATATCAATATCACTGGGGGGAATTTATCTAATGATAAAA	1464
Db	452	ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn	470
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Db	471	LysAsnIlePheGlyLeuProIleLysLysArgArgGluAsnGlnGlyAsnProThrLeu	490

Db	131	SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr	150
Qy	487	TATAAATACAGCATTTAGATGATCGAGAAAATTAATAAGACTACAAAGCTCTCGATTACCA	546
Db	151	TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln	165
Qy	547	CCATCATCAGCATTACACAACAGCTGCTTGACTCTTAAAAATACGATTTGAGAATGTTCCAC	606
Db	166	AsnThrGlnAspValArgThrGlnIleGlnLeuValHisThrHisPheGlnAsnValIle	185
Qy	607	AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACTTCGAACTTATAAAACGCTA	660
Db	186	ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu	205
Qy	661	TTACTCTCTATTATCGCAAGCTGCTAAATTTTCATTAAATTTATTACAAACAGGTGCT	720
Db	206	ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValIleAsnGlnAlaVal	225
Qy	721	GAATTCGGCTGATGAATGGAAATGCAGATATACATCTCTTCAAAATGAACCTAATGCTGGA	780
Db	226	LysPheGluAlaTyrIleLysAsnAsnArgGlnPheAspTyrIleuGluPro---LeuPro	244
Qy	781	ACATCAGATGACATTTATTAACCTTTTAAAGAAAATATATACCTTAATATAGTACTATTGT	840
Db	245	ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys	264
Qy	841	GCAAAATACCTATAGAGAGGACTAAATAAACTTCGAAACGAACT-----	885
Db	265	ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp	284
Qy	886	---AATATGAGATGGAGTATTAATATGATATTCGAGATATATGACTATTACTGTATTA	942
Db	285	GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu	304
Qy	943	GATACTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGATTCATATAGGAAGA	1002
Db	305	AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle-----	320
Qy	1003	ATAGGTGGCATTAATAACTGAACTTACAAGAGAAATTTATACAACCTGAATAATTTTGAC	1062
Db	321	-----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu	337
Qy	1063	CGTCTTACTTCTGAAATTCACCCCACTCTCGCTATAATGGAATATATATTAACACCGT	1122
Db	338	GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg	355
Qy	1123	TCAGGGCTGAGATATTTTCATTTTAGATGAACCTTATATTTATACAAAATAATGAACG	1182
Db	356	ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr	374
Qy	1183	TACGGGAATCGTTAGTTGGTATTCGGAATCGTAATAGATCTACTTATGCT-----	1233
Db	375	ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn	393
Qy	1234	ACGACAGGAACCTGAAATTTATATATGAGAGAAACAGGCTCCACCACCAACAAAATTTTA	1293
Db	394	IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu	413
Qy	1294	ATACCAATTTGAATCCTATAAAGTTTCAATTTGTAATCTGATAGACAGTAACCTCTACTTC	1353
Db	414	-----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn	431
Qy	1354	CTTTTCCTTAACATATCTTTACAAATTAATCAAAATGAACTTTTAAATTAATTAATCACCT	1413
Db	432	LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr	451
Qy	1414	-----AGTAATAAAATTAACATATCAATATCAAGCTGGGGGGAATTTATCTAATGATA	1464
Db	452	ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn	470
Qy	1465	ACAACCTGATTTTCAATTTCTGTAAAAAAGACTGTAAACCAATATTAATTAATCCTAATGT	1524
Db	471	LysAsnIlePheGlyLeuProIleLysLysArgArgGluAsnGlnGlyAsnProThrLeu	490

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QY 1525 TTACCAAGCTAATAGTATTAGTATCATATTTTATCCAGATTCTCTTTATTAATTAT--- 1581
Db 491 PheProThrTyraAspAsnTySerHisIleLeuSerPheIleLysSerLeuSerIlePro 510
QY 1582 ---TCTATAAAATGGATTAGCGCTAAATATATTATATACAGGTGCATTAGGATGGACA 1638
Db 511 AlaThrTyrlsA-----ThrGlnValTyrlsPheAla-----TrpThr 523
QY 1639 CACAGTAGCTTAATAGAAATATCCATATACAGATAAAATAATATACATGATCCAGCA 1698
Db 524 HisSerSerValAspProLysAsnThrIleTyrlsHisLeuThrGlnIleProAla 543
QY 1699 ATCAAAGGTACAGCTTGTGATCAAACTCTAAGGTAAATGAAGGACCTGGTCATACAGGA 1758
Db 544 ValIlysaLAsnSerLeuGlyThrAlaSerLysValGlnGlyProGlyHisThrGly 563
QY 1759 GGAACCTGGTTTATTTACAAAGTCNAGGGCGCTTTAGAGATTACATGATAGAACTCCTAAT 1818
Db 564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
QY 1819 TCTACACAATCTTATACATTAGCTTCGATACGCTACAAATAGGTGCTGGAAATCTCTT 1878
Db 582 PheGlnGlnSerTyrlsPheIleArgIleArgTyrlsAlaSerAsnGlySerAlaAsnThrArg 601
QY 1879 CCTAATATATCTCTTACAACTCCAGGAGTAATAGGAATACCACCTCAACGACTCAACAAC 1938
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620
QY 1939 ACTTTTCTGGTACAAAATTAATAATTTACAATACGGAGATTTTGGGTATTTCGAATTT 1998
Db 621 ThrPheSerGlyThrAspTyrlsAsnLeuLysTyrlsAspPheGlnTyrlsLeuGluPhe 640
QY 1999 CCAAGTACAGTAACATTAACCTTTAAATCGAAACATACCATTAATTAATTAATCGTCAGAT 2058
Db 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
QY 2059 GTA---TCAAAATCAATTTAATCATATGATAAAATTTGAATTTATACCAATTAATCTCT 2115
Db 661 ValTyrlsAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
QY 2116 GTACGCCAAAATAGAGAAAACAAAATTAGAAACTATCCAAACAAAATAATAATACATTT 2175
Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAsnThrPhe 700
QY 2176 TTCACAATCATACAAAATAACTTTAATATATATAGAGCCAAACATATGATATTCAT 2232
Db 701 TyrlsAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrlsAspIleAsp 719

RESULT 2
Q7AL67_BACTI PRELIMINARY; PRT; 1180 AA.
AC Q7AL67;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Pesticidal crystal protein cry4AA.
GN Name=cry4AA; Synonym=cryIVA(A), IsrH4, pBt110;
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1430;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22235415; PubMed=12324359;
RX DOI=10.1128/AEM.68.10.5082-5095.2002;
RA Berty C., O'Neil S., Ben-Dov E., Jones A.P., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.,
RT "Complete sequence and organisation of ptxois, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 68:5082-5095(2002).
DR EMBL; AL731825; CAD30148.1; -; Genomic DNA.
SQ SEQUENCE 1180 AA; 134538 MW; 6FB5B6979DACAD3B CRC64;

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Alignment Scores:
Pred. No.: 5,16e-70 Length: 1180
Score: 1158.00 Matches: 283
Percent Similarity: 54.55% Conservations: 131
Best Local Similarity: 37.29% Mismatches: 281
Query Match: 29.40% Indels: 64
DB: 2 Gaps: 25

US-10-782-570-1 (1-2325) x Q7AL67_BACTI (1-1180)
QY 13 AATAATAATGAATAGATTAATGATTCATCGATTCA-----AGAATTTATCTTATCTCTTCTAAC 66
Db 6 AsnLysAsnGluTyrlsGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
QY 67 AGAAATATTGATCATCTTAGTAGTACCTTACACAATAATCAACAATCAACCAATCAACAAAC 126
Db 26 -----TyrThrArgTyrlsProIleGluAsnSerProLysGlnLeuGlnSer 41
QY 127 ACAATTAACAAGAGTGGCTCAATATGTCTCAAGGAATACACAATATATGATGATAATTTTC 186
Db 42 ThrAsnTyrlsAspTrpLeuAsnMetCysGlnGlnAsnGlnGlnTyrlsGlyAspPhe 61
QY 187 GAGACATTTGCTAGTCTGATCAATGCTCTGCTGCTAGTTCAGGTACTATTGTTATCCGGT 246
Db 62 GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrlsThrIleValValGly 78
QY 247 ACTCTGTTAGCCGCTATAGTGGGCTCACTTCTATATCCGACCGCATAGGAATAATAGGT 306
Db 79 ThrValLeuThrGlyPheGlyPheThrThr-----ProLeuGlyLeu----- 92
QY 307 GCTATAATAATATCTTTTGGTACCTTAATCACTACTGCTTTTGGCCCGCGGAGAACACAGAC 366
Db 93 ---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111
QY 367 AAAACAGTATGACACAAATTTATTAATAATGGGAGAAATTTTGTGTGATACACCGTTAACA 426
Db 112 AsnThr---TrpSerAspPheIleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
QY 427 GAAACATAAACACAGCTAAAGTTACAACTTTAGNAGGATTTAGACAATATTACAAAGC 486
Db 131 SerThrTyrlsSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150
QY 487 TATTAATACAGCATATAGATGATTGGAGAAAATTTAAAAGACTACAAGCTCTCGATTACCA 546
Db 151 TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln 165
QY 547 CCATCATCAGCATTTACAAACAGCTGCCTTGAATACGATTTGAGATGATGTTAC 606
Db 166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrlsHisPheGlnAsnValIle 185
QY 607 AATGATTTTATTCGGAATAATACCT-----GGTTTCCAATTTGAACCTTATAAAGCGTAA 660
Db 186 ProGluLeuValAsnSerCysProAsnProSerAspCysAspTyrlsAsnLeuLeu 205
QY 661 TTACTACCTATTATTATGCGCAAGCTCTAATTTTCAATTTTAAATTTATTAACAACAGGTGCT 720
Db 206 ValLeuSerSerTyrlsAlaGlnAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal 225
QY 721 GAAATGGCTGATGATGGAATGCAGATATACATCTCTTCAAAATTTGAACCTTAATGCTGGA 780
Db 226 LysPheGluAlaTyrlsLeuLysAsnAsnArgGlnPheAspTyrlsLeuGluPro---LeuPro 244
QY 781 ACATCAGATGATATTAATAACTTTTAAAGAAATATACCTTAATATAGTAACTATTGCT 840
Db 245 ThrAlaIleAspTyrlsProValLeuThrLysAlaIleGluAspTyrlsThrAsnTyrlsCys 264
QY 841 GCABAATCTTATAGAGAGGACTAAATAAACTTCGAAAACGAACT----- 885
Db 265 ValThrThrTyrlsLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
QY 886 ---AATATGAGATGGAGTATATTTAATGATTATTCGAAGATATATGACTATTACTGTTATA 942
Db 886 ---AATATGAGATGGAGTATATTTAATGATTATTCGAAGATATATGACTATTACTGTTATA 942

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285	Gly	Asn	Leu	Asn	Trp	Asn	Thr	Tyr	Asn	Thr	Tyr	Arg	Thr	Leu	Leu	Val	Leu	304
943	GAT	A	C	T	A	T	C	G	C	T	C	A	A	T	T	C	T	1002
305	Asp	Leu	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Val	Gly	Leu	Pro	Leu	Pro	320	
1003	AT	A	G	G	T	G	C	A	T	T	A	A	A	C	T	T	1062	
321	----	Gly	Val	Gln	Ser	Glu	Leu	Thr	Arg	Glu	Leu	Leu	Tyr	Gln	Val	----	337	
1063	CGT	C	T	T	A	C	T	T	G	A	A	T	C	A	C	C	1122	
338	Glu	Ser	Pro	Tyr	Leu	Tyr	Tyr	----	Asp	Phe	Gln	Tyr	Gln	Glu	Asp	Ser	355	
1123	TC	A	G	G	G	T	T	A	G	A	T	T	T	T	A	G	1182	
356	Arg	Pro	----	His	Leu	Phe	Thr	Trp	Leu	Asp	Ser	Leu	Asn	Phe	Tyr	Glu	374	
1183	T	A	C	G	G	A	T	C	G	T	T	T	G	G	A	T	1233	
375	Thr	Pro	Asn	Asn	Phe	Phe	----	Thr	Ser	His	Tyr	Asn	Met	Phe	His	Tyr	393	
1234	AC	G	A	C	A	G	A	C	T	G	A	A	A	A	G	A	1293	
394	I	Leu	Ser	Gln	Leu	Ser	Ser	Val	Phe	Gly	Asn	His	Asn	Val	Thr	Asp	413	
1294	A	T	A	C	A	T	T	G	A	A	T	T	C	A	A	T	1353	
414	----	Gly	Leu	Ala	Thr	Asn	Leu	Tyr	Leu	Phe	Leu	Leu	Asn	Val	Leu	Asp	431	
1354	C	T	T	T	T	C	T	A	C	A	T	A	T	A	T	T	1413	
432	Leu	Ser	Leu	Asn	Asp	Tyr	Asn	Asn	Leu	Ser	Leu	Met	Asp	Phe	Phe	Leu	451	
1414	----	Arg	T	A	T	A	A	T	T	A	C	A	T	T	T	C	1464	
452	Arg	Leu	Leu	Glu	Leu	Ser	Glu	Leu	Thr	----	Ala	Gly	Ser	Gly	Leu	Thr	470	
1465	A	C	A	C	T	G	A	T	T	T	C	G	T	A	A	A	1524	
471	Leu	Asn	Leu	Phe	Gly	Leu	Pro	Leu	Leu	Leu	Arg	Arg	Glu	Asn	Gln	Leu	490	
1525	T	T	A	C	A	A	G	T	A	T	A	T	A	T	T	T	1581	
491	Phe	Pro	Thr	Tyr	Asp	Asn	Tyr	Ser	His	Leu	Ser	Phe	Leu	Ser	Leu	Ser	510	
1582	----	TC	C	T	A	T	A	A	A	T	T	G	A	T	T	A	1638	
511	Ala	Thr	Tyr	Leu	----	----	Thr	Gln	Val	Tyr	Thr	Phe	Ala	----	Trp	Thr	523	
1639	C	A	C	A	G	T	A	G	T	A	A	T	A	T	A	A	1698	
524	His	Ser	Val	Asp	Pro	Leu	Ser	Asn	Thr	Leu	Tyr	Thr	His	Leu	Thr	Gln	543	
1699	A	T	C	A	A	G	T	A	A	C	T	T	C	T	A	C	1758	
544	Val	Leu	Ala	Asn	Ser	Leu	Gly	Thr	Ala	Ser	Leu	Val	Val	Gln	Gly	Pro	563	
1759	G	A	A	A	C	T	T	G	T	T	A	T	T	A	C	A	1818	
564	Gly	Asp	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	581	
1819	T	C	T	A	C	A	A	T	T	A	C	T	T	A	C	T	1878	
582	Phe	Gln	Gln	Ser	Tyr	Phe	Leu	Arg	Gly	Arg	Tyr	Ala	Ser	Asn	Gly	Ser	601	
1879	C	C	T	A	A	T	A	T	C	T	T	A	C	A	T	A	1938	
602	Ala	Val	Leu	Asn	Leu	Ser	Leu	Pro	Gly	Val	Ala	Glu	Leu	----	Gly	Met	620	
1939	A	C	T	T	T	T	C	T	G	T	A	C	A	A	T	T	1998	
621																		

Qy	1999	CCAAAGTACAGTAACATTCACCTTTAAATTCGAAACATACCAATTTATTTATTTATCTGTGCAGAT	2058
		:::	
Db	641	SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnA-GSerAsp	660
		:::	
Qy	2059	GTA---TCAAAATTCAAATTTAACTGATATAAAATTCGAATTTATACCAATTACTTCTCT	2115
		::   :::	
Db	661	ValTyrThrAsnThrValLeuIleAspGlyIleGluPheLeuProIleThrA-gSer	680
		::   :::	
Qy	2116	GTACGCCAAATAGAGAAAAACAAAATATAGAACTATCCAAACAAAAATAATACATTT	2175
		:::	
Db	681	IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAsnThrPhe	700
		::   :::	
Qy	2176	TTCACAATCATACAAAAATACTTTAAATATATAGAGCCCAAACTATGATATTTGAT	2232
		:::	
Db	701	TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp	719
		::   :::	
RESULT 3			
Q9FDC0_BACTF			
ID	Q9FDC0_BACTF	PRELIMINARY;	PRT; 1128 AA.
AC	Q9FDC0;		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Parasporal inclusion protein Cry.		
GN	Name=cry;		
OS	Bacillus thuringiensis (subsp. finitimus).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;		
OC	Bacillus cereus group.		
OX	NCBI_TaxID=29337;		
FN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Moore G.D., Debro L.H.;		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF285775; AAG00235.1; -; Genomic_DNA.		
DR	HSSP; Q06117; 1J16.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	GO; GO:0030435; P:sporulation; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SEQ	SEQUENCE 1128 AA; 127450 MW; 61B0DC9454BDF0B8 CRC64;		
Alignment Scores:			
Pred. No.:	5.79e-53	Length:	1128
Score:	906.50	Matches:	245
Percent Similarity:	49.44%	Conservative:	108
Best Local Similarity:	34.31%	Mismatches:	242
Query Match:	23.01%	Indels:	119
DB:	2	Gaps:	28
US-10-782-570-1 (1-2235) x Q9FDC0_BACTF (1-1128)			
Qy	199	AGTCTGATACAAATTCGTGAGTGTAGTGCAGGTPACTATTGTATCCGTACTCTGTGTAGCC	258
		::   :::	
Db	28	SerSerAspThrValAlaValValSerAlaGlyIleValValGlyThrIleLeuThr	47
		::   :::	
Qy	259	GGTATAGTGGGCTCACTTCTATATCCGGACCGATAGGAATATATAGGTGTATAATAATA	318
		::   :::	
Db	48	-----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle	60
		::   :::	
Qy	319	TCITTTGGTACCCTTAATCACTGTCTTTTCGCCCGCGGAGAACAGAC---AAACAGTA	375
		::   :::	
Db	61	SerPheGlyThrIleuAlaProValLeuThrProAspProGluGluAspProLysLysIle	80
		::   :::	
Qy	376	TGGACACAAATTTTAAATATGGGAGAAATTTTGTGTGATACACCGTTAAACAGAAACATA	435
		::   :::	

Db 81 TrpSerGlnPheMetLysHisGlyGluAspLeuLeuAenGlnThrIleSerThrAlaVal 100  
Qy 436 AAACAGCTAAAGTTTACAACTTTAGAGGATTTAGACAAATATATACAAAGCTTATAATACA 495  
Db 101 LysGluIleAlaLeuAlaHisLeuAenGlyPheLysAspValLeuThrTyrrTyrrGluArg 120  
Qy 496 GCATTAGATGATTGGAGAAAATTAATAAGAGACTACAAGCTCTCGGATTACCAACCATCATCA 555  
Db 121 AlaPheAenAspTrpLysArg-----AsnProSerAla 131  
Qy 556 GCATTACAAACAGCTGCTTACTTCTTAAATATACGATTTGAGAAATGTTTCACATGATTTT 615  
Db 132 -----AsnThrAlaArgLeuValSerGlnArgPheGluAenAlaHisPheAenPhe 148  
Qy 616 ATTGCAGAAATACCTGGTTTCCAACTCGAACTTATAAAACGCTATTACTACTACTATTAT 675  
Db 149 ValSerAenMetProGlnLeuGlnLeuProThrTyrrAspThrLeuLeuLeuSerCysTyrr 168  
Qy 676 GCGCAAGCTGCTAAATTTTCAATTAAATTTATTAACAAGGTCGTGGAATTTGGCTGATGAA 735  
Db 169 ThrGluAlaAlaAenLeuHisLeuAenLeuHisGlnGlyValGlnPheAlaAspGln 188  
Qy 736 TCGAATGAGATATACATCTCTTCAAAATTTGAACCTAATGCTGGAAATCATGATGACTAT 795  
Db 189 TrpAenAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr-----Tyr 205  
Qy 796 TATAAATTTTAAAGAAATATACCTAAATATAGTAACTATGTCGAAATACCTATAGA 855  
Db 206 TyrAspGluLeuValTyrrIleGlnLysTyrrIleAenTyrrCysThrLysThrTyrrHis 225  
Qy 856 GAAGACTAAATATAAATTCGAACCGAATCTAATATGAGATGAGTATATTAATGATTTAT 915  
Db 226 LysGlyLeuAenHisLeuLysGluSerGluLysIleThrTrpAspAlaTyrrAsnThrTyrr 245  
Qy 916 CGAATATATAGACTATATCTGTATATAGTATCTATGCTCAATTTCTTTTATGATATA 975  
Db 246 ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyrrAspIle 265  
Qy 976 AAGAGATACAAGATTCAATAGGAGATAGTGGCATTAAACTGAACTTACAGAGAA 1035  
Db 266 ArgArgPhePro-----ArgGlyValGluLeuGluLeuThrArgGlu 279  
Qy 1036 ATTATACAACT-----GAAATAAATTTT 1059  
Db 280 ValTyrrThrSerLeuAspProGlyLeuAenAlaGlyProIleProGluIleAspPhe 299  
Qy 1060 GACCGCTTACTTACTTACCTTGAATTCACCCCAATCTCGCTATAATGGAATATAATTAACA 1119  
Db 300 -----SerTyrrLeuGluAspHisLeuThr 307  
Qy 1120 CGTTCAGGCTTAGATTTTTCATTTTGTAGATGAACTTATATTTTATACAAAATGAA 1179  
Db 308 ArgProPro-----GlyLeuPheThrTrpLeuSerAspIleGluLeuTyrrThrGluSerVal 326  
Qy 1180 ACGTACGGGAATCGTTTGTAGTTGGAATCGTAATAGATCTACTTACTTATGCTACGACA 1239  
Db 327 AlaGluGlyAspTyrrLeuSerGlyIle-----ArgGluSerLysTyrrTyrrThr 342  
Qy 1240 GGAACCTGAAAT-----ATATATGAGAAAGAACAGGTCACCCCAACA 1284  
Db 343 GlyAenGlnPhePheThrMetLysAenIleTyrrGlyAen-----ThrAen 357  
Qy 1285 AAA-----ACTTTATACATTTTGAATCTCTATAAGTTTCAATTTGTA 1326  
Db 358 ArgLeuSerLysGlnLeuIleThrLeuLeuProGlyGlu-----PheIleThrHisLeuSer 376  
Qy 1327 ACTGATGACAAAGTAACCTCTACTTCCCTTTTCTCAATATATCTTTTCAATTAATCAA 1386  
Db 377 IleAenArgGlyPheGlnThrIleAlaGlyIleAenLysLeuTyrrSerLeuIleGlnLys 396  
Qy 1387 ATTGAATCTTTATTTAAATTAATTCACCTAGTAAATTAATTAACATATTTACAGCTGGGGGAAT 1446  
Db 397 Ile-----ValPheThrThrPheLysAenAspAenGluTyrrGlnLysAenPheAen 413

Qy 1447 TTATCTAATGAT-----AAAAAACCACTGATTTTCAATTTTCTCTGTAATAAACAC 1497  
Db 414 ValAenAenGlnAenGluProGlnGluThrThrAenTyrr----- 426  
Qy 1498 TGTAAACCAATTTAATTAATTTCAAAATTTGTTTCAAGCTATATAAGT-----TATAGTCAT 1551  
Db 427 -----ProAenAspTyrrGlyGlySerAenSerGlnLysPheLysHis 440  
Qy 1552 ATTTTATCCAGTTTCTTTTATTTAATTTATTTCTTATATAAATTTGGATTAGCGCTAAATATA 1611  
Db 441 AenLeuSerHisPheProLeuIleIleHisGlnValGluPheAlaGluTyrrPheHisSer 460  
Qy 1612 TTATATACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1671  
Db 461 IlePhe-----AlaLeuGlyTyrrThrHisAenSerValAenSerGlnAenLeuIleSer 478  
Qy 1672 GATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1731  
Db 479 GluSerValSerThrGlnIleProLeuValLysAlaTyrrGluValThrThrAenSer--- 497  
Qy 1732 GTAAATTGAAGCAGCTGCTCATACAGGAGAACTTGGTTTATTTTACAAAGTCAGGGCGT 1791  
Db 498 VallleargGlyProGlyPheThrGlyGlyAspLeuIleGluLeuArgAsp-----Lys 515  
Qy 1792 TTAGAGATTACATGTAAGAACTCTTAATTTCTACACAACTTATTTACATTTAGCTTCGATAC 1851  
Db 516 CysSerIleLysCysLysAla---SerSerLeuLysLysTyrrAlaIleSerLeuPheTyrr 534  
Qy 1852 GCTCAAAATGCTGCGAAATACCTCTTCTTAATATATCTTTTACAAATACCAAGGAGTAATA 1911  
Db 535 AlaAlaAenAenAlaIleAlaValSerIleAspValGlyAspSerGlyAlaGlyValLeu 554  
Qy 1912 GGAATACCACTCAACGACTCAACAACTTTTCTGTCATCAAAATTTATAATAAT----- 1965  
Db 555 -----LeuGlnProThrPheSerArgLysGlyAenAenAenPheThr 568  
Qy 1966 -----TTCAATACGAGATTTTGGTATTTTCCAAATTTTCCAAAGTACATCACTA 2016  
Db 569 IleGlnAspLeuAenTyrrLysAspPheGlnTyrrHisThrLeuLeuValAspIleGluLeu 588  
Qy 2017 CCTTTAAATCGAAATACATACCATTTTATATTTTATCTGTCAGAT-----GTATCAAAATCA 2070  
Db 589 ProGluSerGluGluIleHisIleHisLeuLysArgGluAspAspTyrrGluGluGlyVal 608  
Qy 2071 ATTTTATCATTTGATAAATTTGAATTTTATACCAATTTACTTCTCTGTAGCCAAAATAGA 2130  
Db 609 IleLeuLeuIleAspLysLeuGluPheLysProIleAspGluAenTyrr-----Thr 625  
Qy 2131 GAAAAACAAAAATTAGAACTATCCAAACAAAAATAAATACATTTTTCACAAATCATACA 2190  
Db 626 AenGluMetAenLeuGluLysAlaLysLysAlaValAenValLeuPheIleAenAlaThr 645  
Qy 2191 AAAAATCTTTAAATATAGAACCCCAAACTATGATATTGAT 2232  
Db 646 ---AenAlaLeuLysMetAspValThrAspTyrrHisIleAsp 658

## RESULT 4

C28AA BACTF STANDARD; PRT; 1109 AA.  
ID C28AA BACTF AC Q9X682;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Pesticidal crystal protein cry28Aa (insecticidal delta-endotoxin  
DE CryXXVIIIa(a)) (Crystalline entomocidal protoxin) (126 kDa crystal  
DE protein).  
GN Name=cry28Aa; Synonyms=cryXXVIIIa(a);  
OS Bacillus thuringiensis subsp. finitimus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=29337;  
RN [1]



Db 452 ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla 471  
Qy 1708 AACAGCTCTTGATACAACTTAAGCTTAATGAGGAGCTGTCATACAGGAGGAACTTG 1767  
Db 472 TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyGlyAspLeu 490  
Qy 1768 GTTATTATTACAAAGTCAAGGGCTTTAGAGATTCATGATGAGATCCCTAAATTCACACA 1827  
Db 491 IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys 507  
Qy 1828 TCTTATTACATTAGACTTCGATACCTACAAATGCTGCGAAATACCTCTTCCTTAATATA 1887  
Db 508 LysTyrAlaIleSerLeuPheTyrAlaAlaAsnAsnAlaIleAlaValSerIleAspLeu 527  
Qy 1888 TCTCTTCAATACACGAGGATATAGATATACCACTCAACGACTCAACACACATTTTCT 1947  
Db 528 GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer 541  
Qy 1948 GGTACAAATATAATAAT-----TTACAATACGGAGATTTTGGGTATTTTC 1992  
Db 542 ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyrLysAspPheGlnTyrHis 561  
Qy 1993 CAATTTCCAAAGTACGATACATCTTTAAATCGAAACATACCACTTTATATTTAATCGT 2052  
Db 562 ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisIleHisLeuLysArg 581  
Qy 2053 CGAGAT-----GTATCAAAATCAATTTTATCATGTATATAAATTTGAATTTATACCAAT 2106  
Db 582 GluAspAspTyrGluGluGlyValIleLeuLeuIleAspLysLeuGluPheLysProIle 601  
Qy 2107 ACTTCTCTGTACGCAAAATAGAGAAACAAATAATTTAGAACTATCCAAACAAATAA 2166  
Db 602 AspGluAsnTyr-----ThrAsnGluMetAsnLeuGluLysAlaLysLysAlaVal 618  
Qy 2167 ATACATATTTTCCAAATCATACAAATAATCTTTAAATATATAGAGCCCAAACTATGAT 2226  
Db 619 AsnValLeuPheIleAsnAlaThr---AsnAlaLeuLysMetAspValThrAspTyrHis 637  
Qy 2227 ATGAT 2232  
Db 638 IleAsp 639

## RESULT 5

C10AA\_BACTI STANDARD; PRT; 675 AA.  
AC P09662;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Pesticidal crystal protein cry10Aa (Insecticidal delta-endotoxin  
DE CryXA(a)) (Crystalline entomocidal protoxin) (78 kDa crystal protein).  
GN Name=cry10Aa; Synonyms=cryIVc, cryXA(a);  
OS Bacillus thuringiensis subsp. israelensis.  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1430;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=ONR60A;  
RX MEDLINE=86233796; PubMed=3011746;  
RA Thorne L., Garduno F., Thompson T., Decker D., Zounes M., Wild M.,  
RA Walfield A.M., Pollock T.J.;  
RT "Structural similarity between the lepidoptera- and diptera-specific  
RT insecticidal endotoxin genes of Bacillus thuringiensis subsp.  
RT 'kurstaki' and 'israelensis'";  
RL J. Bacteriol. 166:801-811(1986).  
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
CC epithelial cells of mosquitoes. Active on Aedes aegypti.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.

CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; M12662; AAA22614.1; -, Genomic\_DNA.  
DR PIR; B29838; B29838.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin C.  
DR InterPro; IPR005639; endotoxin N.  
DR Pfam; PF03944; Endotoxin C; 1.  
DR Pfam; PF00555; Endotoxin M; 1.  
DR Pfam; PF03945; Endotoxin N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 675 AA; 77761 MW; 2A70011BEA7985F5 CRC64;  
  
Alignment Scores:  
Pred. No.: 2,4e-52 Length: 675  
Score: 897.00 Matches: 251  
Percent Similarity: 47.96% Conservative: 114  
Best Local Similarity: 32.98% Mismatches: 268  
Query Match: 22.77% Indels: 128  
DB: 1 Gaps: 32  
  
US-10-782-570-1 (1-2235) x C10AA\_BACTI (1-675)  
Qy 13 AATATATATGATATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 72  
Db 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25  
Qy 73 ATTGATCATTTAGTATACCTTACCAATATCAATATCAATATCAATATCAATATCAATATCAAT 132  
Db 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43  
Qy 133 TACAAGAGTGGCTCAATATGTCACGGGATATACCAATATGATGATGATGATGATGATGATGATGAT 192  
Db 44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnTyrGlyAsnAsnAlaGlyAsn 63  
Qy 193 TTTGCTAGTCTGATACAAATTTGCTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 252  
Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83  
Qy 253 TTAGCCGTATAGTGGGCTCACTCTATATCCGACCGATAGGATATAGTGTGTATATAGTGTGTATAT 312  
Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95  
Qy 313 ATAATATCTTTTGTACCTTAATCACTGCTTTTGGCCGCGGAGAGAACAGACAAACAA 372  
Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp-----GlnGlySerAspProAlaAsn 114  
Qy 373 GTATGGACACAAATTTATTAAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAA--- 429  
Db 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130  
Qy 430 -----AGCATATAAACAGCTTAAGTTACAACTTTAGAGAGGATTTAGACAAATATATACAA 483  
Db 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150  
Qy 484 AGCTATATATACAGCATTTAGATGATTTGGAGAGAAATTTAAAGAGACTCAAGCTCTCGATTATA 543  
Db 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163  
Qy 544 CCACCATCATCAGCATTAACCAAGCTGCTTGAATCTTTAAATACGATTTGAGATGTT 603  
Db 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181  
Qy 604 CACAAT-----GATTTTATTCGAGAAATACCTGTTTCCAACTTGAACATTATATAA 654  
Db 182 IleAspLysAspLeuAspMetLeuLysAsnAlaSerTyrArgIleProThr----- 199

QY 655 ACGCTATTACTACCTATTATGCGCAAGCTGCTAATTTTTCATTTAAATTTTATTACACAA 714  
 Db 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216  
 QY 715 GGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCCACAAATTTGAACCTAAT 774  
 Db 217 AlaAlaThrTyrTyrAsnIleTrp -----LeuGlnAsnGlnGlyIleAsnProSer 233  
 QY 775 GGTGGAACATCAGATGACTATTATAAA---CTTTTAAAGAAAATATACCTAAATATATAGT 831  
 Db 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253  
 QY 832 AACTATTCTGCAAAATACCTATAGAGAAGGACTTAATAACTTCGAAACCAACCTAATATG 891  
 Db 254 AspTyrCyHisIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273  
 QY 892 AGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACATATC 951  
 Db 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293  
 QY 952 GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAAATAGGTGCG 1011  
 Db 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307  
 QY 1012 ATTAAACTGAATCTACAGAGAAATTTATACACTGAAATTAATTTTGACCGTCTTACT 1071  
 Db 308 ValLysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326  
 QY 1072 TACCTTGAAATTCACCCCAATCTCGCTATATGGAATATAATTTAAACACGTTTACGGGCTT 1131  
 Db 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339  
 QY 1132 AGATTATTTTCATTTTATAGTGAATCTATATTTTATACAAAAAT- 1176  
 Db 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359  
 QY 1177 GAAACGTATAC-----CGGAATCGTTTGTAGTTGGTATTGCGAATCGTAAAT 1218  
 Db 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373  
 QY 1219 AGATCTACTTGTCTACGACAGGAATCGAAATTTATATATGAGAAAGAACAGGT----- 1272  
 Db 374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392  
 QY 1273 ---CCACCCACACAAAACTTTAATACATTTGAAATCCAT-----AAAGTT 1317  
 Db 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412  
 QY 1318 TCATTTGTAAGTATGATACAGAGTAACCTCTACTCCCTTTTCTTCAATATATCTTTACA 1377  
 Db 413 GluIleValArgHisArgGlu-----TyrSerAsp 422  
 QY 1378 ATTAATCAAAATGAATCTTTTAAATTAATTAATCACTAGTATAATAATTAACATATTCAGCT 1437  
 Db 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441  
 QY 1438 GGGGGGAATTTATCTAATGATATAAAAAACAATGATTTTCAATTTTCCCTGTATAAAAAAGAC 1497  
 Db 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461  
 QY 1498 TGTAACCAATTTAATCCAAATTTGTTTACCAAGCTATAATAGTATTAGTCATATTTTA 1557  
 Db 462 TrpLys-----AsnGluGluTyrGlyHisThrLeu 471  
 QY 1558 TCCACGATTTTCTTTTATTTAATTTTCCATATAAATTTGGATTAGCGCTAAATATATATAT 1617  
 Db 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg 488  
 QY 1618 ACAGGTGCATAGGATGACACACAGTATGTTTAAATAGAAATAATGCAATATCAGATAAA 1677  
 Db 489 ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508  
 QY 1678 ATAATTACATGATCCCGAGCAATCAAGGTAAACAGTCTTGTGTATACAAATCTCAAGTAAAT 1737

Db 509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528  
 QY 1738 GAAGACCTGCTCATACAGAGAAACTTGTTTATTATACAAAGTCAAGGCGGTTTAGAG 1797  
 Db 529 LysGlyProGlyHisThrGlyGlyAspLeuValIleLeuLysAspSer-----MetAsp 546  
 QY 1798 ATTACATGTAGA---ACTCCTAAATTTCTACAAATCTTATACATAGTACTTCGATACGCT 1854  
 Db 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566  
 QY 1855 ACAAATCGTCTCGAATAACTCTCTCTTAATATATCTCTTACAAATACCAAGGAGTAATAGGA 1914  
 Db 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581  
 QY 1915 ATACCACCTCAACGACTCAACACACTTTTCTGGTACAAATATAAT-----AATTTA 1968  
 Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600  
 QY 1969 CAATACGAGGATTTGGGTATTTCCAAATTTCCAAAGTACAGTA----- 2010  
 Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620  
 QY 2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTATTCGTGCAGATGTA 2061  
 Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635  
 QY 2062 TCAAAATCAATTTTAAATCATTGATAAATTTGAATTTATACCAATTTCTCTCTGTACGC 2121  
 Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654  
 QY 2122 CAAAATAGAGAAAAACAAAATAGAACTATCCAAACAAAAATAATACATTTTTCACA 2181  
 Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674  
 QY 2182 AAT 2184  
 Db 675 Asn 675  
 RESULT 6  
 Q8KNV2\_BACTI PRELIMINARY; PRT; 675 AA.  
 ID Q8KNV2; BACTI PRELIMINARY; PRT; 675 AA.  
 AC Q8KNV2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Peptidicidal crystal protein cry10AA.  
 GN Name: cry10AA; Synonyms: cryIVC, cryXA(A), pBt047;  
 OS Bacillus thuringiensis (subsp. israelensis).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1430;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22235415; PubMed=12324359;  
 RX DOI=10.1128/AEM.68.10.5082-5095.2002;  
 RA Barry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,  
 RA Harris D., Zaritsky A., Parkhill J.;  
 RT "Complete sequence and organisation of pBtoxis, the toxin-coding  
 RT plasmid of Bacillus thuringiensis subsp. israelensis.";  
 RL Appl. Environ. Microbiol. 68:5082-5095(2002).  
 DR EMBL; AL731825; CAD30098.1; -; Genomic DNA.  
 DR GO; GO:0016787; F1hydrolase activity; IEA.  
 DR GO; GO:0005102; F1receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR GO; GO:0030435; P:sporulation; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.

SQ SEQUENCE 675 AA; 77759 MW; 4EB0851AA0372FF1 CRC64;

## Alignment Scores:

Pred. No.: 2.4e-52 Length: 675  
Score: 897.00 Matches: 251  
Percent Similarity: 47.96% Conservative: 114  
Best Local Similarity: 32.98% Mismatches: 268  
Query Match: 22.77% Indels: 128  
DB: 2 Gaps: 32

US-10-782-570-1 (1-2235) x 08KNV2\_BACTI (1-675)

QY 13 AATAATATGAATATGATGATATTCGATTCAGAAAGATTTATCTTATCTTCTTCAACAGAAAT 72  
DB 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25  
QY 73 ATTGATCAATTCAGATACCTTACACAATATCAATCAACATTCACCAATTCACAAACAAT 132  
DB 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43  
QY 133 TACAAGAGTGGCTCAATATGTCACAGGGATACACAATATGGTGATATTCGAGACA 192  
DB 44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnTyrGlyAsnAlaGlyAsn 63  
QY 193 TTTCGTAGTGTGATACAAATTCGCTGAGTGTAGTGTAGTGTATGATTCGGTACTCTG 252  
DB 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83  
QY 253 TTAGCCGGTATAGTGGGCTCACTCTATATCCGACCGCATAGGAAATATAGGTGCTATA 312  
DB 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95  
QY 313 ATAATATCTTTGGTACCTAATCACTGCTTTTGGCCGGGAGAGAACACACAAACA 372  
DB 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp-----GlnGlySerAspProAlaAsn 114  
QY 373 GTATGGACACAATTTATTAAATGGGAGAAATTTTGTGTATACACCGTTAACAGAA--- 429  
DB 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130  
QY 430 -----AGCATAAACACAGCTAAGTTACAACTTTAGAGAGGATTTAGCAATATTACAA 483  
DB 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150  
QY 484 AGCTATATACAGCATGATGATGAGAGAAATTTAAAGACACACAGCTCTCGATTA 543  
DB 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163  
QY 544 CCACCATCATCAGCATTAACAACAGCTGCTTGAAGCTCTTAAATACGATTTGAGAAATGT 603  
DB 164 -----ThrHleAlaAsnAlaLysAlaValHleAspLeuPheThrThrLeuGluProIle 181  
QY 604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAA 654  
DB 182 IleAspLysAspLeuAspMetLeuLysAsnAlaSerTyrArgIleProThr----- 199  
QY 655 AGCTATTACTACTATTTATCGCAGCTGCTTAATTTTCATTTTAAATTTATACACA 714  
DB 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHleAsnLeuLeuLysHis 216  
QY 715 GGTGCTGAATTCGGCTGATGAATGATGATGATATACATCTTCCAAATTCGAACCTAAT 774  
DB 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233  
QY 775 GCTGGAACATCAGATCTATTATATAA-----CTTTTAAAGAAATAATATACCTAAATAGT 831  
DB 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253  
QY 832 AACTATTGTGCAATACCTATAGAGAGGACCTAAATAACTTCGAAACGACCTAATAG 891  
DB 254 AspTyrCysIleGlnThrThrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273  
QY 892 AGATGGAGTATATTTAATGATTTATCGAAGATATATGACTATTACTGTATTAGTATATC 951

DB 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293  
QY 952 GCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAGAAATAGGTGCG 1011  
DB 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307  
QY 1012 ATTAAACTGAACCTTACAGAGAAATTTATACAACTGAAATATAATTTTTCACGCTCTTACT 1071  
DB 308 ValLysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326  
QY 1072 TACCTTGAAATTCACCAATCTCGCTATATAAGATATATAATTTAACAGCTTCAGGGCTT 1131  
DB 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339  
QY 1132 AGATTATTTTCATTTTAGAGTAACTTATATTTTATACAAAAAT----- 1176  
DB 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359  
QY 1177 GAAACGTAC-----GGGAATCGTTTGTAGTTGGTATTTCGGAATCGTAAT 1218  
DB 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373  
QY 1219 AGATCTACTTATGCTACGACAGAACTGAAATATATATATGAGAAAGAACAGGT----- 1272  
DB 374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392  
QY 1273 ---CCACCCACACAAAACCTTTAATACCATTTGNAATCTAT-----AAAGTT 1317  
DB 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412  
QY 1318 TCAATTTGTAACGTAGATAGACAAAGTAACTCTACTCTCCCTTTTCTTAAACATATCTTTACA 1377  
DB 413 GluIleValArgHisArgGlu-----TyrSerAsp 422  
QY 1378 ATTAATCAAAATTGAACCTTTTATTAATAATTAATCACTAGTAAATAATTAACATATTACGT 1437  
DB 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441  
QY 1438 GGGGGGAATTTATCTAATGATATAAACAACACTGNTTTTCAATTTCTCTGTAATAAAGAC 1497  
DB 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461  
QY 1498 TGTAAACCAATTTATTAATCCAAATTTGTTTACCAAGCTATAATAGTATTAGTCATATTTTA 1557  
DB 462 TrpLys-----AsnLysGluTyrGlyHisThrLeu 471  
QY 1558 TCCCAAGTTTCTTTTATTTTATTTCTTATATAAATTTGGATTAGCGCTAAATATATATAT 1617  
DB 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg 488  
QY 1618 ACAGGTGCATTTAGGATGGACACACAGTAGTGTGTTAATAGAAATAATGCAATATACATAAA 1677  
DB 489 ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508  
QY 1678 ATAATTACAATGATCCCAAGCAATCAAGGTAAACAGCTCTTGATACAAACTCTAAGGTAAT 1737  
DB 509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528  
QY 1738 GAAGACCTGGTCATACAGGAGAACTTGGTTTATTTTACAAGTCACAGGGCGTTTAGAG 1797  
DB 529 LysGlyProGlyHisThrGlyAspLeuValIleLeuLysAspSer-----MetaAsp 546  
QY 1798 ATTACATGTAGA---ACTCCTTAATCTACACAACTCTTATTAATAGTCTTCGATACGCT 1854  
DB 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566  
QY 1855 ACAATGGTGTGGAAATACTCTCTCTAATATATCTCTTACAAATACAGGAGTAATAGGA 1914  
DB 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581  
QY 1915 ATACCACCTCAACGACTCAACACACTTTTCTGTTACAAATTAATAAT-----AATTTA 1968

Db	44	TyrIysAspTrpThrAsnMetCysAlaIleAspAsnAsnLeuIysSerIleAsnProPhe	63
QY	187	GAGACATTTGCTAGTGTGATACAAATGCTGCAGTTAGTCAGGTACTATTGTATCCGGT	246
Db	64	GluaAsnLeuGlnAsnSerLeuValGlyLeuPheAlaIleThrAlaIleAlaSer	83
QY	247	ACTCTGTTAGCCGGTATAGTGGGCTCACTTCTATATCCGAGCCGATAGGAATAGAGT	306
Db	84	LeuLeuSerAlaProIleThrGlyGlyThrSerIleAlaAalagLyThrAlaIleAlaAa	103
QY	307	GCTATAATAATATCTTTTGGTACCTTAATACATGCTCTTTTGGCCCGGGAGAACAGAC	366
Db	104	AlaIleIleProIleLeuTrpProSerIleProIleLeuTrpProSerIleProIleLeu	114
QY	367	AAAACAGTATGGACACAAATTTATAAATGGGAGAAATTTTCTGTGATACACCGTTAAAC	426
Db	115	AsnAsnLeuProAspIysLeuLeuAlaIleSerGluaIleThrLeuTyrSerPheGlnAsp	134
QY	427	GAAGACATAAAACAGCTAAAGTTTACAACTTTTAGAAGGATTTAGACAAATATTACAAAGC	486
Db	135	GlnArgValArgGluaAspAlaLeuThrArgLeuGluSerLeuIysAspSerValIysTyr	154
QY	487	TATAATACAGCATTAGTAGTTGGAGAAATTTAAAAGACTACAGCTCTCGGATTACCA	546
Db	155	PheGluAsnAlaPheThrPheTrpIleAsn-----Asn	165
QY	547	CCATCATCAGCATTTACAAACAGCTGCTTGACTCTTAAATACAGATTGAGAAATGTTCCAC	606
Db	166	ProAsnSerThr-----AsnThrThrThrValArgGluArgPheGlnGluValAsn	182
QY	607	AATGATTTTATTCGAGAAATPACCTGGTTTCCAACTTTGAAACTTATAAAAGCTATTACTTA	666
Db	183	GlyArgPheValGlySerMetAlaPhePheArgAlaIysAsnTyrGluProIleLeuLeu	202
QY	667	CCTATTTCGCGAAGCTGCTAAATTTTCATTTAAATTTATTACAAAGGTCGTGAATTG	726
Db	203	SerThrTyrAlaGlnAlaArgLeuHisLeuHisLeuAspGlyIleThrTyr	222
QY	727	GCTGATGAATGAATGCAGATATACATCCTTCACAAATGAACTTAATGCTGCGAACATCA	786
Db	223	AlaGluIysTrpAsnLeuSerArgGlnGlyAspAspMet-----ProGly	237
QY	787	GATGACTATTATAAACTTTTAAAGAAAAATATACCTAAATATAGTAACATTATGTCGAAAT	846
Db	238	AspLeuLeuTyrIysGluPheAsnLysTyrCysAsnGluTyrIleGluHisCysIleLys	257
QY	847	ACCTATAGAAAGACTAAATAAACCCTCGAAACGAACCTTAATATGATAGGAGTATATTT	906
Db	258	TrpTyrAsnGluSerLeuSerLeuLeuLysSer--ValGlyAlaAsnTrpLeuGluTyr	276
QY	907	AATGATTATCGAAGATATAGCTATTACTGTATTATAGATACTACCTCAATTTCTTTT	966
Db	277	AsnGlnTyrArgThrPheLeuThrAlaSerValLeuAspValIleSerLeuPheSerSer	296
QY	967	TATGATATAAGAGATACAAAGATTCAATGAGGAAGAAATAGGTGGCACTTAAACTGAACCT	1026
Db	297	TyrAspProArgLeuTyrIysGluArgLeuSer-----ValGluIleLeu	311
QY	1027	ACAAGAGAAATTTATCAACTGAAATAAATTTTGGCCGCTTACTTACTACCTTGAAATTCAA	1086
Db	312	ThrArgIysLeuTyrThrAspProIleAsnTyrHisArgGlyIleSerLeuAlaAsp	331
QY	1087	CCCAATCTCGCTATATGGAATATATTTTAAACAGTTTCAGGGCTTAGATATTTCATTT	1146
Db	332	GluSer-----LysTyrThrLeuGluProThr-----LeuPheThrGln	344
QY	1147	TTAGATGAACCTTATTTTATACAAAAATGAAACCTAGCGGAATCGTTTAGTTGGTATT	1206
Db	345	LeuTyrThrLeuThrPheTyrSer--AsnIlePheTyr-----AsnTyrMetGlyHis	361
QY	1207	CGCAATCGTAAATAGATCTACTTATGCTACGACAGGAACCTGAAATTTATATATGAGAAAGA	1266
Db	362	ThrAsn-----ThrTyrArgTyrLeuSerProAspIysIlePheAlaGluArg	377

QY	487	TATAATACAGCATTAGATGATTTGGAGAAATTTAAAGACTACAAAGCTCTCGGATTACCA	546
DB	155	PhleuAsnAlaPheThrPheTrpIleAsn-----	Asn 165
QY	547	CCATCATCAGCATTACAAACAAGTCGCTTGGCTCTTAAATACGATTTCGAGATGTTCCAC	606
DB	166	ProAsnSerThr-----AsnThrThrValArgGluArgPheGlnGluValAsn	182
QY	607	AATGATTTTATTCGAGAAATACCTGGTGTTCCTTCCAACTTGAACCTTATAAAACGGCTATTACTA	666
DB	183	GlyArgPheValGlySerMetalaPhePheArgAlaIysAsnTyrgluProIleLeuLeu	202
QY	667	CCTATTATTCGCGAAGTCGTCAATTTTCATTAAATTTATTACAACAAGSGTCGTGAATTG	726
DB	203	SerThrTyralaGlnalaalaaArgLeuHieLeuHieLeuAspGlyIleThrTy	222
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QY	787	GATGACTATTATAAACTTTTAAAAAGAAATATACCTTAAATATAGTAACCTATTCTGCAAAAT	846
DB	238	AspLeuLeuTyrlsGluPheAsnLysTyrcysAsnGluTyrlleGluHieCysIleLys	257
QY	847	ACCTATAGAGAAGACTAAATAAACCCTCGAAACGAACCTAATATGATGAGATGAGATATTT	906
DB	258	TrpTyraAsnGluSerLeuSerLeuLeuLysSer---ValGlyAlaAsnTrpLeuGluTy	276
QY	907	AATGATTTATCGAAGATATATGACTATTACTGTATTATAGACTACTCGCTCAATTTCTTTT	966
DB	277	AsnGlnTyraArgThrPheLeuThrAlaSerValLeuAspValIleSerLeuPheSerSer	296
QY	967	TATGATATAAAGAGATACAAAGATTCCAATGAGGAAGAAATAGTGGCATTTAAAACTGAACCT	1026
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QY	1027	ACAAGAGAAATTTATCAACTGAAATATAATTTTGGACGCTTACTTACTACCTTGAAATTCAA	1086
DB	312	ThrArgLysLeuTyrlsThrAspProIleAsnTyrcysHieArgGlyIleSerLeuAlaAsp	331
QY	1087	CCCAATCTCGCTATATGGAATATATTTTAAACAGTTTCAGGGCTTAGATTTTTCATTT	1146
DB	332	GluSer-----LysTyrlsThrLeuGluProThr-----LeuPheThrGln	344
QY	1147	TTAGATGAACCTATTATTTATACAAAAATGAAACGTACGGGAATCGTTTAGTTGGTATT	1206
DB	345	LeuTyrlsThrLeuThrPheTyrlsSer---AsnIlePheTyrls-----AsnTyrlsMetGlyHie	361
QY	1207	CGCAATCGTAAATAGATCTACTTATGCTACGACAGGAACCTGAAATTTATATATGAGAAAGA	1266
DB	362	ThrAsn-----ThrTyraArgTyrlsLeuSerProAspLysIlePheAlaGluArg	377

155	Db	PhelUasnAlaPheThrPheThrPileAsn-----Asn	165
547	Qy	CCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAANATACGATTTGAGATGTCAC	606
166	Db	ProAsnSerThr-----AsnThrThrValArgGluArgPheGlnGluValAsn	182
607	Qy	AATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAAGCGCTATTACTA	666
183	Db	GlyArgPheValGlySerMetalPhePheArgAlaLysAsnTyrGluProIleLeuLeu	202
667	Qy	CCTATTATTCGCGCAAGCTGCTAAATTTTCAATTTTAAATTTTATTAACAACAGGTGCTGAATTG	726
203	Db	SerThrTyrAlaGlnAlaAlaArgLeuHisLeuLeuHisLeuArgAspGlyIleThrTyr	222
727	Qy	GCTGATGATGGAATGCAGATATACATCCCTTCAAAATTTGAACCTTAATGCTGGAAACATCA	786
223	Db	AlaGluLysTrpAsnLeuSerArgGlnGlyAspMet-----ProGly	237
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238	Db	AspLeuLeuTyrLysGluPheAsnLysTyrCysAsnGluTyrIleGluHisCysIleLys	257
847	Qy	ACCTATAGAGAAGACTAAATAAACCTTCGAAACGAAACCTAAATATGATGAGTGGAGTATT	906
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907	Qy	AATGATTCGAAGATATATGACTATTACTGTATTATAGTACTATCGCTCAATTTTCTTTT	966
277	Db	AsnGlnTyrArgThrPheLeuThrAlaSerValLeuAspValIleSerLeuPheSerSer	296
967	Qy	TATGATATAAGAGATACAAAGATTCAATAGGAAAGAAATAGTGGCATTAATACTGAACCTT	1026
297	Db	TyrAspProArgLeuTyrLysGluArgLeuSer-----ValGluIleLeu	311
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312	Db	ThrArgLysLeuTyrThrAspProIleAsnTyrHisArgGlyIleSerLeuAlaAsp	331
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332	Db	GluSer-----LysTyrThrLeuGluProThr-----LeuPheThrGln	344
1147	Qy	TTAGATGAACCTTATATTTATACAAAAATGAAACCTACGGGAATCGTTAGTTCGTATT	1206
345	Db	LeuTyrThrLeuThrPheTyrSer---AsnIlePheTyr-----AsnTyrMetGlyHis	361
1207	Qy	GCGAATCGTAAATAGACTACTTATGCTACGACAGGAACCTGAATATATATATGAGAAAGA	1266
362	Db	ThrAsn-----ThrTyrArgTyrLeuSerProAspLysIlePheAlaGluArg	377

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Qy	::        ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::	1026
Db	297 TyrAspProArgLeuTyIryIySgluArgLeuSer-----ValGluIleLeu	311
Qy	1027 ACAAGAGAAATTTATCAACTGAANAATAATTTGACCGCTTACTTACCTG	1086
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Qy	1207 GCGAATCGTAAATAGACTCTTATGTGTACGACAGGAACCTGAAATTTAT	1266
Db	362 ThrAsn-----ThrrTyrrGtyrLeuSerProAspIySleIlePheAlaGlu	377









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 DT 10-MAY-2005 (TREMELrel. 30, Last sequence update)  
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 DE Pesticidal crystal protein cry4BA.  
 GN Name=cry4BA; Synonyms=B78, cryD2, cryIVB(A), IserH3, pBt038;  
 OS Bacillus thuringiensis (subsp. israelensis).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 CX NCBI\_TaxID=1430;  
 RN [1]  
 RP MEDLINE=223235415; PubMed=12324359;  
 RX DOI=10.1128/ASM.68.10.5082-5095.2002;  
 RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,  
 RA Harris D., Zaritsky A., Parthill J.,  
 RT "Complete sequence and organisation of pBtoxis, the toxin-coding  
 RT plasmid of Bacillus thuringiensis subsp. israelensis."  
 RL Appl. Environ. Microbiol. 68:5082-5095 (2002).  
 DR EMBL; AL731825; CAD30095.1; -; Genomic DNA.  
 SQ SEQUENCE 1136 AA; 127763 MW; 8AC4E8C26FE3E9B5 CRC64;

Alignment Scores:  
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 QY 139 GAGTGGCTCAATATGTCTCAAGGGAATACACAATATGTGTATATTTTCGAGACATTTGCT 198  
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 QY 259 GGTATAGGTGGTCTCACTCTTATATCCGACCGATAGGAATAATAGTGTCTATTAATA 318  
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 QY 376 TGGACACAAATTTTAAATGGGAGAAATTTTGTGATACACCGTTTAAACAGAAAGCAT 435  
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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
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GN Name=Cry30Aa;
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OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
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RA Delecluse A., Ordaz S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
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DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
SQ SEQUENCE 688 AA; 77844 MW; 780D57085BD7B3A9 CRC64;

Alignment Scores:
Pred. No.: 7.18e-46 Length: 688
Score: 801.50 Matches: 244
Percent Similarity: 46.82% Conservative: 109
Best Local Similarity: 32.36% Mismatches: 272
Query Match: 20.35% Indels: 129
DB: 2 Gaps: 30

US-10-782-570-1 (1-2235) x Q8VNX1_BACTV (1-688)
Qy 13 AATAATATGAATATGATATATCGAT---TCAAAGAATTTATCTTCTCTTAACAGA 69
Db 6 AsnLysAsnGluTyThrGluIleLeuAspThrSerGlnLysAsnSerAsnMetSerAsnArg 25
Qy 70 AATATTGATCATTTAGATACCCCTTACACAAAATAATCAAAATCAACCATTAACAAACACA 129
Db 26 -----TyrSerLysTyThrProLeuThrAsnAsnProLysValProLeuGlnAsnThr 42
Qy 130 AATTACAAGAGCGCTCAATATATGTGTCAAGGGGATACACATATGTTGATATTTTCGAG 189
Db 43 AsnTyThrLysAspTrpLeuAsnMetCysGlnThrIleThrProLeuCysThrProIleAsp 62

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D	b		272	ThrAsnIleSerTrpGlyThrTy rAsnLysTyrArgArgGluValThrLeuGlyAlaLeu	291
Q	y		943	GATACTATCGCTCAATTTCTTTTATAGATATAAAGAGATACAAAGANTCAAATAGGAAGA	1002
D	b		292	AspLeuAlaAlaLeuPheProAsnTyrAspIleCysileTyrProIleGln-----	308
Q	y		1003	ATAGGTGGCATTAATAACTGNACTTCAAGNAGAATTTATACAACACTGAAATAAATTTTGAC	1062
D	b		309	-----ThrLysThrGluLeuThrArgLysValTyrMetProSerPheGlyLeuGln	325
Q	y		1063	CGTCTTACTTACCCTTGAAATTCAACCCAATCTCGCTATATATGAATGAATTAATTTAAACACGT	1122
D	b		326	GlnSerAsnTyrPheGln-----SerLeuGluGlyLeuGluAsnAlalaLeuThrHis	342
Q	y		1123	TCAGGGCTTAGATATTATTTTCATTTTAGATGAACATTATATTTATACAAAAATGAAACG	1182
D	b		343	ProPro--SerLeuPheThrTrpLeuAsnGluLeuAsnLeuTyrThrIleArgGluAsn	361
Q	y		1183	TACGGG-----AATCGTTTAGTTGGTATT-----	1206
D	b		362	PheAsnProAlalaLeuLeuValSerSerLeuSerGlyLeuGlnAlalaIleSerArgTyrThr	381
Q	y		1207	GCGAATCGTAAATAGACTACTTATGCTACGACAGGAACTGAAATATATATATGCGAAGA	1266
D	b		382	GlnAsnProAsnArgIleSerAsnProAlaGlnGlyVal-----Arg	395
Q	y		1267	ACAGGTCACCCACAACAAAACCTTTAATACCACTTTGAAATCTTATAAAGTTTCAATTTGTA	1326
D	b		396	AsnGlyThrProThrGlnIleGlyLeuAsnAsnLeuPheValTyrLysLeuSerLeu---	414
Q	y		1327	ACTGATAGACAAGTAACCTCTACTTCCCCTTTT-----CCTAACATATATCTTTTACAAT	1380
D	b		415	-----SerGlnTyrHisHisProAsnGluCysTyrSerIle	426
Q	y		1381	AATCAAATT-----GAACCTTTATAATAATTTCCACTGAGTAAT	1419
D	b		427	AlaGlyIleSerAspMetThrPheTyrLysSerAspTyrAsnGlyAsnAlalaProThrThr	446
Q	y		1420	AAATTAACATATTCCAGCTGGGGGAATTTATCTAATCATATAAAAAACAACCTGATTTTCAA	1479
D	b		447	Gln---ThrTyrGlnAlaGlyArgAsn--SerAsnAsnPheIleAsnThrPheMetAsn	464
Q	y		1480	TTTCCTGTAAAAAAGACTGTAAACCAATTTAATCAAAATGTTTACCAGAGCTATAAT	1539
D	b		465	GlyProGlnGluAlaSerSerSerAsnAsnIle-----SerIleLys	478
Q	y		1540	AGTTATAGTCATATTTTTATCCAGTTTCTTTATTATTATTTATCCCTATAAAATGGATT	1599
D	b		479	GlnThrAsnHisIleLeuSerAspIleLysMetIle---TyrSerArgThrGlyGlyThr	497
Q	y		1600	CGCGTAATATATATATACAGGTGCATTAGGATGGACACACAGTACTGTGTTAATAGAAAT	1659
D	b		498	TyrProSerTyrAspPheGlyTyrSerPheAlatrphThrHisThrSerValAsnProAsp	517
Q	y		1660	AATGCAATATCACATAAAAAATTTACAATGATCCAGCAATCCAAGTAGTAACAGCTTGAT	1719
D	b		518	AsnLeuIleValProAsnArgIleThrGlnIleProAlaValLysAlaAspTyrLeuThr	537
Q	y		1720	ACAACCTCTAAGGTAAATGAAGACCTGGTCATACAGAGGAACTTGGTTTATTTA---	1776
D	b		538	SerProAlaLysValIleAlaGlyProGlyHisThrGlyGlyAspLeuValAlaLeuLeu	557
Q	y		1777	-----CAAAGTCAAGCGGTTTAGAGATTACATGTAGAACTCCTAAATCTTACA---	1824
D	b		558	AsnAlalaThrGlnAlaGlyArgMetGlnIleGlnCysylsThrGlySerPheThrGly	577
Q	y		1825	-----CAATCTTATTACATTAGACTTTCGATACGCTCAAAATGGTGT-----	1866
D	b		578	AlaSerArgArgTyrGlyIleArgIleArgTyrAlaAlaAsnAlalaLeuThrValSer	597
Q	y		1867	-----GGAAATACTCTTCTCTAATATATCTCTTACATACCAGGA	1905
D	b		598	LeuSerTyrThrValGlnGlyGlyAsnThrMetSerThrThrPheIleThrGluArgThr	617



QY 1906 GTAATAGGATACCACTCAAGCTCAACACACTTTTCTGGTACAAAATTAATAAT 1965  
 Db 618 PheLeu- - - - - ArgProAenAenThrIlePro- - - - - ThrAsp 628  
 QY 1966 TTACATACCGAGATTTTGGGTATTTCCAATTTCCAACT- - - - - ACAGTAACATTACCT 2019  
 Db 629 LeuIysTyrGluGluPheLysTyrLysGluTyrAenGlnIleIleThrMetThrAlaPro 648  
 QY 2020 TTAATCGAAACATACCACTTTATATTTAATCGTGCAGATGTA- - - - - TCAAATTCAAATTTA 2076  
 Db 649 GlnAenThrIleValThrIleAlaIleGlnLeuAenAlaPheProAenAspGlnLeu 668  
 QY 2077 ATCATTTGATAAATGAATTTATACCAATTTACTTCCTCTGTA 2118  
 Db 669 IleIleAspAArgIleGluPheTyrProMetAspGlnGlyVal 682

RESULT 14  
 ID C19BA\_BACUH STANDARD; PRT; 682 AA.  
 AC O86170;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Pepticidal crystal protein cry19Ba (Insecticidal delta-endotoxin  
 DE CryXIXB(a)) (Crystalline entomocidal protoxin) (78 kDa crystal  
 DE protein).  
 GN Name=cry19Ba; Synonyms=cryXIXB(a);  
 OS Bacillus thuringiensis subsp. higo.  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=132266;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RA MEDLINE=98369730; PubMed=9704107;  
 RX Hwang S.H., Saitho H., Mizuki E., Higuchi K., Ohba M.;  
 RT "A novel class of mosquitocidal delta-endotoxin, Cry19B, encoded by a  
 Bacillus thuringiensis serovar higo gene.";  
 RL Syst. Appl. Microbiol. 21:179-184(1998).  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of mosquitoes.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; D88381; BAA32397.1; -; Genomic\_DNA.  
 DR HSSP; Q06117; IJ16.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; Endotoxin C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid; Sporulation; Toxin.  
 SQ SEQUENCE 682 AA; 78491 MW; 5351EA63E2B042F7 CRC64;

## Alignment Scores:

Pred. No.:	1.34e-39	Length:	682
Score:	709.00	Matches:	239
Percent Similarity:	44.79%	Conservative:	109
Best Local Similarity:	30.76%	Mismatches:	283
Query Match:	18.00%	Indels:	146
DB:	1	Gaps:	35

US-10-782-570-1 (1-2235) x C19BA\_BACUH (1-682)

QY 13 AATAATATGAATATGATTCGATTCAAAG- - - AATTATCTTATCTCTTAAACAGA 69  
 Db 6 AsnLysAenGluTyrGluIleLeuAspAlaLysAenThrCysHisMetSerAsn- - - 24  
 QY 70 AATATGATCATCTAGATACCTTACCAAAATCAAAATCAACCATCAACAAACACA 129  
 Db 25 - - - - - CysTyrProLysTyrProLeuAlaAsnAspProGlnMetTyrLeuArgAsnThr 42  
 QY 130 AATTACAAAGGCGCTCAATATGTCGCAAGGGNATACACAATATGCTGATAATTCGAG 189  
 Db 43 HisTyrLysAspTyrPheAenMetCysGluGlu- - - - - Ala 54  
 QY 190 ACATTTCTAGTGTGATACAAATTCGTCAGTTAGTCAGGTACTATTGTATCCGCTACT 249  
 Db 55 SerTyrAlaSerSerGlyProSerGlnLeuPheLysValGly- - - - - GlySer 70  
 QY 250 CTGTTAGCCGGTATAGTGGGCTCATTCTATATCCGGACCGATAGGAATAATAGGTGCT 309  
 Db 71 IleValAlaLysIleLeuGlyMetIleProGluValGlyProLeu- - - - - 85  
 QY 310 ATAATAATATCTTTTGGTACCCCTAAATCACTGCTCTTTTGGCCGCGGAGAACAGACAAA 369  
 Db 86 - - - - - LeuSerTrpMetValSerLeuPheTrpProThrIleGluGluLysAsn 101  
 QY 370 ACAGTATGACACACAATTTATTAATGGGAGAAATTTTCTTGATACACCGTTAACAGAA 429  
 Db 102 ThrValTrpGluAspMetIleLysTyrValAlaAsnLeuLeuLysGlnLeuThrAsn 121  
 QY 430 AGCATAAACAGCTAAAGTTACAAACTTTAGAGAGATTAGACAAATATTACAAAGCTAT 489  
 Db 122 AspThrLeuAsnArgAlaThrSerAsnLeuSerGlyLeuAsnGluSerLeuAsnIleTyr 141  
 QY 490 AATACAGCATAGTATGTCGAGAAATTAATAAGACTACAAGCTCCTCGATTACCACCA 549  
 Db 142 AsnArgAlaLeuAlaIleTrpLysGlnAsnLysAsnAsnPheAlaSerGly- - - - - 158  
 QY 550 TCATAGCATTACAAACAGCTGCTTGAACCTTTAAATATCGATTTCGAAATGTTCACAAT 609  
 Db 159 - - - - - GluLeuIleArgSerTyrIleAsnAspLeuHisIle 170  
 QY 610 GATTTTATTCGAGAAATACCTGGT- - - TTCCAACTTGAACCTTATAAAGCTATTACTA 666  
 Db 171 LeuPheThrArgAspIleGlnSerAspPheSerLeuGlyTyrGluThrValLeuLeu 190  
 QY 667 CCTATTATCGCAAGCTGCTAATTTTCATTAAATTTATTACAAACA- - - - - 714  
 Db 191 ProSerTyrAlaSerAlaAlaAsnLeuHisLeuLeuLeuArgAspValAlaIleTyr 210  
 QY 715 GGTGCTGAATTTGGCTGATGAATGGAATGCAATATACATCCTTCACAAATTTGAACCTAAT 774  
 Db 211 GlyLysGluLeuGly- - - - - TyrProSerThr- - - - - 219  
 QY 775 GCTGGAACATCAGATGCTATTATAAATCTTTTAAAGAAAATATACCTAATATAGTAAC 834  
 Db 220 - - - - - AspValGluPheTyrAsnGluGlnLysTyrThrGluLysTyrSerAsn 237  
 QY 835 TATTGTGCAAAATACCTATACAGAGAGACTAAATAAATCTTCGAACGAACCTTAATATCAGA 894  
 Db 238 TyrCysValAsnThrTyrLysSerGly- - - - - LeuGluSerLysLysGlnIleGly 254  
 QY 895 TGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTATGTTAGTACTATCGCT 954  
 Db 255 TrpSerAspPheAsnArgTyrArgGluMetThrLeuSerValLeuAspIleValAla 274  
 QY 955 CAATTTCTTTTATGATATAAAGAGATACAAAGATTCATAGAGAGAAATAGGTGGCATT 1014  
 Db 275 LeuPheProLeuTyrAspThrGlyLeuTyrProSerLysAspGlyLysIle- - - HisVal 293  
 QY 1015 AAAACTGAACCTTACAAGAGAAATTTTATACAACTGAAATAAATTTTGACCGCTCTTACTTAC 1074  
 Db 1015 AAAACTGAACCTTACAAGAGAAATTTTATACAACTGAAATAAATTTTGACCGCTCTTACTTAC 1074

Db 294 LysalaGluLeuThrArgGluIleTy-SerAspValIleAen---AspHisValTyGly 312  
Qy 1075 CTTGAATTCACCAATCTCGCTATA-----ATGGATATATAATTTAAACAGTTACGGG 1128  
Db 313 LeuMetVal---ProTyIleSerPheGluHisAlaGluSerLeuTyThrArgArgPro 331  
Qy 1129 CTTAGATTATTTTCATTTTATAGTAACTTATATATTTATACAAAATTTGAAACGTACGGG 1188  
Db 332 ---HisAlaPheThrTrpLeuTyGlyPheArgPheValThrAenSerIleAenSerTrp 350  
Qy 1189 AATCGTTAGTTGGTATTCGGAATCGTAATAGATCTACTTATGCTACGACAGGAACTGAA 1248  
Db 351 ThrPheLeuSerGlyGlyGluAenArg-----TyrPheLeuThrHisGlyGluGly 367  
Qy 1249 ATTATATAT-----GGAGAAAGACAGGTCCACCACACAAACAACTTTA 1293  
Db 368 ThrIleTyAenGlyProPheLeuGlyGlnAaspThrGluTyGlyThrSerSerTy 387  
Qy 1294 ATACCAATTTGAATCC-----TATAAAGTTTCAATTTGTAACCTGATAGACAAGTA 1341  
Db 388 IleAspIleSerAenAenSerSerIleTyAenLeuTrpThrLysAenTyGluTrpIle 407  
Qy 1342 ACTCCT---ACTCCCTC-----TTTCCTAACATATATTACAAATTAATCAATGAA 1392  
Db 408 TyrProTrpThrAspProValAenIleThrLysIleAenPheSerIleThr----- 424  
Qy 1393 CTTTATTAAATATTCACCTAGTATAAATTAACATATTACGCTGGGGGGAATTTATCT 1452  
Db 425 ---AspAenSerAenSerSerGluSerIleTyGlyAla---GluArgMetAen 440  
Qy 1453 AATGATAAAAAACAACTGATTTTCAATTTCTCTGTAATAAAAGACTGTAAACCAATATT 1512  
Db 441 LysProThrValArgThrAspPheAenPheLeuLeuAenArg----- 454  
Qy 1513 AATCAAAATTTGTTTACCAAGCTATATAGTTATAGTATATTTATCCAGTTTCTTTA 1572  
Db 455 AlaGlyAenGlyProThrThrTyAenAspTyAenHisIleLeuSer---TyrMetLeu 473  
Qy 1573 TTTAAT-----TATTCCTATAAATTTGGATTAGCG 1602  
Db 474 IleAenGlyGluThrPheGlyGlnLysArgHisGlyTySerPhe----- 488  
Qy 1603 CTAAATATATATATATACAGGTGCTAGTATAGTACGACAGTAGTGTAAATAGAAATAAT 1662  
Db 489 -----AlaPheThrHisSerSerValAspArgTyAen 499  
Qy 1663 GCAATATCAGATAAAATAATTAACAATGATCCAGCAATCAAGGTAACAGTCTTGATACA 1722  
Db 500 ThrIleValProAspLysIleValGlnIleProAlaValLysThrAenLeuValGlyAla 519  
Qy 1723 AACTCTAAGTAAATGAAGACCTGGTCAATCAGGAGGAACCTGGTTTATTTTACAAAGT 1782  
Db 520 Aen-----IleIleTyGlyProGlyHisThrGlyGlyAspLeuLysLeuGluTy 537  
Qy 1783 CAAGGGCGTTAGATGATACATGTAAGTCTTAATTTCTACAACTCTTATTACATAGA 1842  
Db 538 GluArgPheLeuSerLeuArgIleLysLeu---IleAlaSerMetThrPheArgIleArg 556  
Qy 1843 CTTTCATAGCTACAAATGGTCTGGAATACTCTTCCTTAATATATATCTCTTACAAATCCA 1902  
Db 557 IleArgTyAlaSerAenIleSerGlyGlnMetMetIleAenIleGlyTyGlnAenPro 576  
Qy 1903 GGAGTAATAGGAATACCACTCAACGACTCAACACATCTTTTCTGGTGAATATATAT 1962  
Db 577 ThrTyPheAenIleIleProThr-----ThrSerArgAspTyThr 590  
Qy 1963 AATTTCATACCGAGATTTTGGG-----TATTTCCAAATTTCCA 2001  
Db 591 GluLeuTyPheGluAaspPheGlnLeuValAaspThrSerTyIleTySerGlyGlyPro 610  
Qy 2002 AGTACAGTAACATTAACCTTTAAATCCGAAACATACCACTATTTATATTAATCGTCAGATGTA 2061  
Db 611 Ser-----IleSerSerAenThrLeuTrpLeuAaspAen-----Phe 622

Qy 2062 TCRAATTCAAATTTTAATCAATGATAAAATTCGAATTTATACCAATTCCTCTCTGACGC 2121  
Db 623 SerAenGlyProValIleIleAspLysIleGluPheIleProLeuGlyIleThrLeuAen 642  
Qy 2122 CAAATAGAGAAAACAAAATTAAGAACTATCCAAACAAAATAAATACATTTTTCACA 2181  
Db 643 Gln-----AlaGlnGlyTyAspThrTyAspGlnAenAlaAenGlyMetTyHis 659  
Qy 2182 AATCATCAAAAATACATCT-----TTAAATATAGAAGCCACAAACTAT 2223  
Db 660 GlnAenTySerAenSerGlyTyAsnTyAenGlnGluTyAsnThrTy 676  
RESULT 15  
ID Q56B08\_BACTU PRELIMINARY; PRT; 1169 AA.  
AC Q56B08;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Crystal protein Cry9Db1.  
GN Name=cry9Db1;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DP1019;  
RA Flannagan R.D., Abad A.R.;  
RT "Bacillus Cry9 Family Members."  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY971349; AAX78439.1; -; Genomic DNA.  
SQ SEQUENCE 1169 AA; 132126 MW; 85DC06D5083E3F43 CRC64;  
Alignment Scores:  
Pred. No.: 1.55e-39 Length: 1169  
Score: 708.50 Matches: 225  
Percent Similarity: 43.25% Conservative: 134  
Best Local Similarity: 27.11% Mismatches: 262  
Query Match: 17.99% Indels: 209  
DB: 2 Gaps: 34  
US-10-782-570-1 (1-2235) x Q56B08\_BACTU (1-1169)  
Qy 1 GTGAATCAAAATAATAATAATGATATGATATGATTCGATTCAAGAAATTTATCTTATCCT 60  
Db 1 MetAenArgAenHisGlnAenGluTyGluIleIleAspAlaProHisCysGlyCysPro 20  
Qy 61 TCTAACAGAAATATTGATCATTTCTAGATACCTCTTACACAAATAATCCAAATCAACATT 120  
Db 21 SerAap-----AspValValLysTyProLeuThrAspAspProAenAlaGlyLeu 37  
Qy 121 CAAACACAAATTAACAAAGAGTGGCTCAATATGTCTCAAGGGAATACACAAATATGTTGAT 180  
Db 38 GlnAenMetAenTyLysGluTyLeuGlnMet-----TyrGlyGly 51  
Qy 181 AATTCGAGACATTTGCTGCTGCTATACAAATTCGTCAGTTAGTCAGGTACTATTGTA 240  
Db 52 AspTy-----ThrAapProLeuIleAenProAenLeuSerVal 64  
Qy 241 TCCGGTACTCTGTTAGCCGGTATAGTGGCTCACTTCTATATCCGACCGGATAGGAATA 300  
Db 65 SerGlyLysAaspValIleGlnValGly-----IleAenIle 76  
Qy 301 ATAGTGTCTATAATATATCTTTTGGT----- 327  
Db 77 ValGlyArgLeuLeuSerPhePheGlyPheProPheSerSerGlnTrpValThrValTy 96  
Qy 328 ---ACCTAATCACTGTCTTTTGGCCCGGGAGAACAGACAAACAGTATGGACACAA 384  
Db 97 ThrTyLeuLeuAenSerLeuTrpPro-----AspAapGluAenSerValTrpAapAla 114



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 12, 2006, 06:12:53 ; Search time 184.5 Seconds  
(without alignment)  
10645.112 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaatcaataataataa.....caaatgatattgattaa 2235

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xl  
-O=/cgn2\_1/USPTO\_epool\_p/US10782570/runat\_12012006\_060221\_7509/app\_query.fasta\_1.2375  
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10782570 -CGN\_1\_260 @runat\_12012006\_060221\_7509 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=120 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A Geneseq\_21.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*  
9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3302	99.1	744	ADR89397	Adr89397 AXMI-007.
2	3623	92.0	694	ADR89399	Adr89399 AXMI-007
3	3314	84.1	735	ADR89395	Adr89395 AXMI-006.
4	1159	29.4	1180	Adp93715	Adp93715 Delta-end
5	1158	29.4	1180	ADR89426	Adr89426 cry4aa.1
6	1157	29.4	1016	Adp94035	Adp94035 Delta-end
7	1157	29.4	1180	Adp82589	Adp82589 Insectici
8	1153	29.3	1180	Adp14373	Adp14373 Dipteran
9	1153	29.3	1180	Aar63078	Aar63078 B.t. toxi

10	901	22.9	1109	5	AAE26353	Aae26353 Bacillus
11	901	22.9	1109	7	ADF31302	Adf31302 Bacillus
12	901	22.9	1109	7	ADF31307	Adf31307 Bacillus
13	900	22.8	686	2	AAR63079	Aar63079 B.t. Toxi
14	899	22.8	675	2	AAR14374	Aar14374 Dipteran
15	897	22.8	675	8	ADR89431	Adr89431 cry10Aa.
16	897	22.8	675	9	ADY59866	Ady59866 Bacillus
17	819	20.8	1136	5	AAU76029	Aau76029 Bacillus
18	819	20.8	1136	8	ADR89427	Adr89427 cry4Ba.1
19	819	20.8	1136	9	AEA61391	Aea61391 Bacillus
20	818	20.8	1136	1	AAP93341	Aap93341 Sequence
21	816	20.7	1136	1	AAP82314	Aap82314 Bacillus
22	787.5	20.0	1169	2	AAW06417	Aaw06417 Antiscara
23	772.5	19.6	1095	1	AAP97052	Aap97052 Sequence
24	755	19.2	1178	1	AAP60051	Aap60051 Bacillus
25	716	18.2	1210	5	AAU99256	Aau99256 Bacillus
26	716	18.2	1210	5	ADL15307	Adl15307 B thuring
27	716	18.2	1210	9	AEb45609	Aeb45609 B. thurin
28	709	18.0	682	8	ADR89433	Adr89433 cry19Ba.
29	708.5	18.0	780	9	AEA81472	Aea81472 Bacillus
30	708.5	18.0	1169	9	AEA81468	Aea81468 Bacillus
31	706	17.9	651	2	AAW06460	Aaw06460 BtPGS1208
32	706	17.9	651	2	AAW06419	Aaw06419 Antiscara
33	706	17.9	659	2	AAU23213	Aau23213 Amino aci
34	706	17.9	659	8	ADR89424	Adr89424 cry3Ba.1
35	700	17.8	652	3	AAU23211	Aau23211 Amino aci
36	700	17.8	652	3	AAU70442	Aay70442 Bacillus
37	700	17.8	652	6	ABU09193	Abu09193 Bacillus
38	700	17.8	652	7	ABW01051	Abw01051 Bacillus
39	699	17.7	1206	5	AAU99255	Aau99255 Bacillus
40	699	17.7	1206	8	ADL15305	Adl15305 B thuring
41	699	17.7	1206	9	AEb45607	Aeb45607 B. thurin
42	695	17.6	651	2	AAU33769	Aar33769 Bt isolat
43	693	17.6	652	3	AAU70443	Aay70443 Synthetic
44	693	17.6	652	3	ABU09194	Abu09194 Bacillus
45	693	17.6	652	7	ABW01052	Abw01052 Bacillus

#### ALIGNMENTS

RESULT 1

ADR89397

ID ADR89397 standard; protein; 744 AA.

XX ADR89397;

AC

DT 18-NOV-2004 (first entry)

XX

DE AXMI-007.

XX

KW delta-endotoxin; delta-endotoxin associate polypeptide;

KW expression cassette; transformation; transgenic; plant; bacteria;

KW lepidoptera; coleoptera; pest; pesticide; resistance;

KW pesticidal activity.

XX

OS Bacillus thuringiensis.

XX

FX Key Location/Qualifiers

FT Misc-difference 1 /note= "encoded by GTG"

XX

XX WO2004074462-A2.

XX

PD 02-SEP-2004.

XX

XX 20-FEB-2004; 2004WO-US005829.

XX

PR 20-FEB-2003; 2003US-0448632P.

PR

PR 20-FEB-2003; 2003US-0448633P.

PR

PR 20-FEB-2003; 2003US-0448797P.

PR

PR 20-FEB-2003; 2003US-0448806P.

PR

PR 20-FEB-2003; 2003US-0448810P.

PR

PR	19-FEB-2004; 2004US-00781979.
PR	19-FEB-2004; 2004US-00782060.
PR	19-FEB-2004; 2004US-00782096.
PR	19-FEB-2004; 2004US-00782141.
PR	19-FEB-2004; 2004US-00782179.
PR	19-FEB-2004; 2004US-00782570.
PR	19-FEB-2004; 2004US-00783417.
XX	(ATHE-) ATHENIX CORP.
PA	
XX	
PI	Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX	
DR	WPI; 2004-635574/61.
DR	N-PADB; ADR89396.
XX	
PT	New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT	and polypeptides, useful for killing lepidopteran or coleopter pests or
PT	for producing organisms with pesticide resistance.
XX	
PS	Claim 12; SEQ ID NO 9; 178pp; English.
XX	
CC	This sequence represents an isolated delta-endotoxin. Some of the delta-
CC	endotoxin coding sequences of the invention have alternative start
CC	codons, producing more than one protein from a single open reading frame.
CC	The nucleic acid sequences of the invention are useful in DNA constructs
CC	or expression cassettes for transformation and expression in plants and
CC	bacteria. The nucleic acids and corresponding polypeptides are useful for
CC	killing lepidopteran or coleopteran pests. Compositions containing the
CC	delta-endotoxins of the invention, and methods for their production, are
CC	useful for the production of organisms with pesticide resistance,
CC	specifically bacteria and plants. These organisms are useful for
CC	generating altered or improved delta-endotoxin or delta-endotoxin-
CC	associated proteins that have pesticidal activity, or for detecting the
CC	presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC	nucleic acids in products or organisms.
XX	
SQ	Sequence 744 AB;
Alignment Scores:	
Pred. No.:	0 Length: 744
Score:	3902.00 Matches: 743
Percent Similarity:	100.00% Conservative: 1
Best Local Similarity:	99.87% Mismatches: 0
Query Match:	99.06% Indels: 0
DB:	8 Gaps: 0
US-10-782-570-1 (1-2235) x ADR89397 (1-744)	
QY	1 GTGATCAAATAAATAATGAATATGAGATTTCGATCAAGAATTTTATCTTACTCT 60
Dd	::::
Dd	1 MetAsnGlnAsnAsnAsnGluTyrgluileleAspSerLyAsnLeuSerTyPrPro 20
QY	61 TCCTACAGAAATATTGTATCATCTTAGATACCCTTACACAATATCCAAATCAACCATTA 120
Dd	21 SerAsnArgAsnileAspHiserargTyPrTyThrAsnAsnProAsnGlnProLeu 40
QY	121 CAAAACACAATATACAAAGATGGCTCAATATGTCTCAAGGGAATACACAATATGTGTAT 180
Dd	41 GlnAsnThrAsnTyrlAsgLuTrlPleuasnMetCysGlnglyAsnThrGlnTyrlGlyAsp 60
QY	181 AATTTCGAGACATTTTGCTAGTCTGATACAAATCTCGAGTGTAGTCAGGTACTATTGTA 240
Dd	61 AsnPheGluThrPheAlaSerAlaAspThrIleAlaValSerAlaGlyThrilieVal 80
QY	241 TCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGAATA 300
Dd	81 SerglyThrLeuleualdcylleglylyLeuThrserIleserglyProIleGlylie 100
QY	301 ATAGGTGCTTAAATAATCTTTTGGTACCTCAATCACTGTCTTTTGGCCCGCGGAGAA 360
Dd	101 IleGlyAlalelleIleSerPheGlyThrleulleThrValPheTyPrroAlaGlyGlu 120
QY	361 CAAGACAAAACAGTATGGACACAATTTATTAAAAATGGGAGAAATTTTGTGTATACACGC 420

QY 1501 AAACCAATTATTAAATCCAAATGTTTACCAAGCTATAATAGTTATAGTCAATATTTATCC 1560  
 DB 501 LysProIleIleAsnProAsnCysLeuProSerTyAsnSerTyAsnSerHisIleLeuSer 520  
 QY 1561 CAGTTTCTTTATTTAAATTTCTTATATAAATTTGATTTAGCGCTAAATATATATATATACA 1620  
 DB 521 GlnPheSerLeuPheAsnTySerTyAsnIleGlyLeuAlaLeuAsnIleLeuTyThr 540  
 QY 1621 GGTGCTAGGATGACACACAGTAGTGTCTTAATAGAAATATGCAATATCATCATGATAAATA 1680  
 DB 541 GlyAlaLeuGlyTrpHisSerSerValAsnArgAsnAsnAlaIleSerAsnIleLeu 560  
 QY 1681 ATTCAATGATCCCAAGCAATCAAGGTAAACAGTCTTTGATACAAATCTTAAGGTAAATGAA 1740  
 DB 561 IleThrMetIleProAlaIleIleGlyAsnSerLeuAspThrAsnSerIleValIleGlu 580  
 QY 1741 GGACTGTGTATACAGAGGAAACCTTGTTTATTTTACAAAGTCAAGGGCTTTAGAGATT 1800  
 DB 581 GlyProGlyHisThrGlyAsnLeuValTyLeuGlnSerGlnGlyArgLeuGluIle 600  
 QY 1801 ACATGTAGACCTCTTAATCTTACAAATCTTATTTACATTTAGCTTCGATACGCTACAAT 1860  
 DB 601 ThrCysArgThrProAsnSerThrGlnSerTyTrpIleArgLeuArgTyAlaThrAsn 620  
 QY 1861 GGTGCTGGAATACTCTTCTTAATATATCTTACAAATACCAAGGAGTAAATAGGAATACCA 1920  
 DB 621 GlyAlaGlyAsnThrLeuProAsnIleSerLeuThrIleProGlyValIleGlyIlePro 640  
 QY 1921 CCTCAACGACTCAACACACTTTTCTGTCACAAATTAATAATTAATTAATTAATTAATTAAT 1980  
 DB 641 ProGlnArgLeuAsnAsnThrPheSerGlyThrAsnTyAsnAsnLeuGlnTyGlyAsp 660  
 QY 1981 TTGCGTATTTCCATTTCCAGTACAGTACATTTACCTTTAAATCGAAACATACATTT 2040  
 DB 661 PheGlyTyThrPheGlnPheProSerThrValThrLeuProLeuAsnArgAsnIleProPhe 680  
 QY 2041 ATATTATTCGTCAGATGTATCAATTTCAATTTTAAATCAATTTTAAATTTAAATTTAATA 2100  
 DB 681 IlePheAsnArgAlaAspValSerAsnSerIleLeuIleIleAspValIleGluPheIle 700  
 QY 2101 CCATTTACTCTCTGTAGCCCAATAGAGAAAACAAATTTAGAACTATCCAAACA 2160  
 DB 701 ProIleThrSerSerValArgGlnAsnArgGluLysGlnLysLeuGluThrIleGlnThr 720  
 QY 2161 AAAATAAATACATTTTTCACAAATCATACAAAATATCTTTAAATATAGAGCCCAAC 2220  
 DB 721 LysIleAsnThrPhePheThrAsnHisThrLysAsnThrLeuAsnIleGluAlaThrAsn 740  
 QY 2221 TATGATATTGAT 2232  
 DB 741 TyrAspIleAsp 744

RESULT 2  
 ADR89399  
 ID ADR89399 standard; protein; 694 AA.  
 XX AC ADR89399;  
 XX DB ADR89399;  
 DT 18-NOV-2004 (first entry)  
 DE AXMI-007 alternative protein.  
 XX delta-endotoxin; delta-endotoxin in associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant; bacteria;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.  
 XX OS Bacillus thuringiensis.  
 XX FN WO200407462-A2.  
 XX DB 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.  
 XX 20-FEB-2003; 2003US-0448632P.  
 PR 20-FEB-2003; 2003US-0448633P.  
 PR 20-FEB-2003; 2003US-0448737P.  
 PR 20-FEB-2003; 2003US-0448806P.  
 PR 20-FEB-2003; 2003US-0448810P.  
 PR 20-FEB-2003; 2003US-0448812P.  
 PR 19-FEB-2004; 2004US-00781979.  
 PR 19-FEB-2004; 2004US-00782020.  
 PR 19-FEB-2004; 2004US-00782096.  
 PR 19-FEB-2004; 2004US-00782141.  
 PR 19-FEB-2004; 2004US-00782570.  
 PR 19-FEB-2004; 2004US-00783417.  
 XX (ATHE-) ATHENIX CORP.  
 XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
 FI WPI; 2004-635574/61.  
 XX N-PSDB; ADR89398.  
 DR New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 XX and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.  
 PT Claim 12; SEQ ID NO 11; 178pp; English.  
 PS This sequence represents an isolated delta-endotoxin. Some of the delta-  
 XX endotoxin coding sequences of the invention have alternative start  
 CC codons, producing more than one protein from a single open reading frame.  
 CC The nucleic acid sequences of the invention are useful in DNA constructs  
 CC or expression cassettes for transformation and expression in plants and  
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
 CC killing lepidopteran or coleopteran pests. Compositions containing the  
 CC delta-endotoxins of the invention, and methods for their production, are  
 CC useful for the production of organisms with pesticide resistance,  
 CC specifically bacteria and plants. These organisms are useful for  
 CC generating altered or improved delta-endotoxin or delta-endotoxin-  
 CC associated proteins that have pesticidal activity, or for detecting the  
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 CC nucleic acids in products or organisms.  
 XX Sequence 694 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.37e-296 Length: 694  
 Score: 3623.00 Matches: 694  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.98% Indels: 0  
 DB: Gaps: 0  
 US-10-782-570-1 (1-2235) x ADR89399 (1-694)  
 QY 151 ATGTCTCAAGGATACACAAATATGTCATATTTTCGAGACATTTGCTAGTCTGATACA 210  
 DB 1 MetCysGlnGlyAsnThrGlnTyGlyAsnPheGluThrPheAlaSerAlaAspThr 20  
 QY 211 ATTGCTGCAGTTAGTCAGGTACTATTGTATCCCGTACTCTGTTAGCCGGTATAGTGGG 270  
 DB 21 IleAlaAlaValSerAlaGlyThrIleValSerGlyThrLeuLeuAlaGlyIleGlyGly 40  
 QY 271 CTCATCTTATATCCGACCGATAGGATATAGTGTCTATATATATATATCTTTGGTACC 330  
 DB 41 LeuThrSerIleSerGlyProIleGlyIleIleGlyAlaIleIleSerPheGlyThr 60  
 QY 331 CTAATCAGTCTTTTGGCCGCGGAGAACAGACAAACAGTAGTATGACACAAATTTATT 390  
 DB 61 LeuIleThrValPheTrpProAlaGlyGluGlnAspLysThrValTrpThrGlnPheIle 80  
 QY 391 AAAATGGAGAAATTTTGTGTATACACCGTTTAAACAGAAAGCATAAACAGCTAAAGTTA 450

	Db	81	LysMetGlyGluIlePheValAspThrProLeuThrGluSerIleLysGlnLeuLysLeu	100
	Qy	451	CARACCTTTAGAGGANTTTAGACAATAATTACAAAGCTATATAACAGCATTAGATGATTGG	510
	Db	101	GlnThrLeuGluGlyPheArgGlnIleLeuGlnSerTyrAsnThrAlaLeuAspAspTrp	120
	Qy	511	AGAAAATTTAAAAAGACTACAAGCTCCTGGATTACCACCATCATCAGCAATTACAAGAAGCT	570
	Db	121	ArgLysLeuLysArgLeuGlnAlaProGlyLeuProProSerSerAlaLeuGlnGlnAla	140
	Qy	571	GCCTTGACTCTTAAATACGATTTGAGNAATGTTCAACATGAATTTTATTCGAGAAATACCT	630
	Db	141	AlaLeuThrLeuLysIleArgPheGluAsnValHisAsnAspPheIleArgGluIlePro	160
	Qy	631	GGTTTTCCAACTTTGAAACTTATAAAGCGTATTACTACCTATTTATGCGCAAGCTGCTAAT	690
	Db	161	GlyPheGlnLeuGluThrTyrLysThrLeuLeuLeuProIleTyrAlaGlnAlaAsn	180
	Qy	691	TTTTCAATTAATTTATTACAACAGGTGCTGAAATTGGCTGATGAATGGAATGCAAGATATA	750
	Db	181	PheHisLeuAsnLeuLeuGlnGlnGlyAlaGluLeuAlaAspGluTrpAsnAlaaspIle	200
	Qy	751	CATCCTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAAA	810
	Db	201	HisProSerGlnIleGluProAsnAlaGlyThrSerAspAspTyrTyrLysLeuLeuLys	220
	Qy	811	GAATAATATACCTAAATATAGTAACCTATTGTGCCAATACCTATACAGAGGAGCTAAATAA	870
	Db	221	GluAsnIleProLysTyrSerAsnTyrCysAlaAsnThrTyrArgGluGlyLeuAsnLys	240
	Qy	871	CTTCGAAACGAACTTAATATGAGATGGAGTATATTAAATGATTAATCGAAGATATATGACT	930
	Db	241	LeuArgAsnGluProAsnMetArgTrpSerIlePheAsnAspTyrArgGlyTyrMetThr	260
	Qy	931	ATTACTGTATTAGATACTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAGAT	990
	Db	261	IleThrValLeuAspThrIleAlaGlnPheSerPheTyrAspIleLysArgTyrLysAsp	280
	Qy	991	TCAATAGNAGAATAGTGGCATTTAAACCTGAACCTTACAAGAGAAATTTATACAACTGAA	1050
	Db	281	SerIleGlyArgIleGlyGlyIleLysThrGluLeuThrArgGluIleTyrThrThrGlu	300
	Qy	1051	ATAAATTTTGACCGTCTTACTTACCTTGAATTCCAACCAATCTCGCTATAATGGAATAT	1110
	Db	301	IleAsnPheAspArgLeuThrTyrLeuGluIleGlnProAsnLeuAlaIleMetGluTyr	320
	Qy	1111	AATTTAACAGCTTCAGGCTTAGATTAATTTTCAATTTTAGATGAACCTTATATTTTATACA	1170
	Db	321	AsnLeuThrArgSerGlyLeuArgLeuPheSerPheLeuAspGluLeuIlePheTyrThr	340
	Qy	1171	AAAAATGAAAGCTACGGGAATCGTTTATGTTGGTATTCGGATCGTATAGTACTTACTTAT	1230
	Db	341	LysAsnGluThrTyrGlyLysArgLeuValGlyIleAlaAsnArgAsnArgSerThrTyr	360
	Qy	1231	GCTACGACGAGAACTGAAATTTATATATGAGAGAAAGACAGCTCCACCCACAACAAAACT	1290
	Db	361	AlaThrThrGlyThrGluIleIleTyrGlyGluArgThrGlyProProThrThrLysThr	380
	Qy	1291	TTAATACATTTTGAATCCTATAAAGTTTCAATTTCAATGTAATGACAGTAAGTACTCTTACT	1350
	Db	381	LeuIleProPheGluSerTyrLysValSerIleValThrAspArgGlnValThrProThr	400
	Qy	1351	TCCCCTTTTCTTAACATATCTTTACAAATTAATCAAAATTCGACTTTTATTAATTAATCA	1410
	Db	401	SerProPheProAsnIleTyrPheThrIleAsnGlnIleGluLeuTyrLeuAsnAsnSer	420
	Qy	1411	CCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAATGATAAAAAACAAC	1470
	Db	421	ProSerAsnLysLeuThrTyrSerAlaGlyAsnLeuSerAsnAspLysLysThrThr	440
	Qy	1471	GATTTTCAAATTTCTGTAAAAAAAGACTGTAACCAATTTAATCAAAATTTGTTTACCA	1530

Db	441	AspPheGlnPheProValLysLysAspCysLysProIleIleAsnProAsnCysLeuPro	460
Qy	1531	AGCTATAATAGTTATAGTCATATTTTATCCAGTTCCTTTTATTAATATTCTCTATAA	1590
Db	461	SerTyrAsnSerTyrSerHisIleLeuSerGlnPheSerLeuPheAsnTyrSerTyrLys	480
Qy	1591	ATTGGATTACGCGTAAATATATTATATACAGGTGCATTAGGATGGACACACAGTAGTGT	1650
Db	481	IleGlyLeuAlaLeuAsnIleLeuTyrThrGlyAlaLeuGlyTrpThrHisSerSerVal	500
Qy	1651	AATAGAAATATTCGATATACAGATAAATATATACATGATCCAGCAATCAAGGTAAAC	1710
Db	501	AsnArgAsnAsnAlaIleSerAspLysIleIleThrMetIleProAlaIleLysGlyAsn	520
Qy	1711	AGTCTTCATCAAACTCTAAGGTAAATTGAAGGACCTGGTTCATACAGGAGAACTTGGTT	1770
Db	521	SerLeuAspThrAsnSerLysValIleGlyGlyProGlyHisThrGlyGlyAsnLeuVal	540
Qy	1771	TATTTACAAAGTCAAGGCGCTTTAGAGATTACATGTAGAACTCCTAATTTCTACACAATCT	1830
Db	541	TyrLeuGlnSerGlnGlyArgLeuGluIleThrCysArgThrProAsnSerThrGlnSer	560
Qy	1831	TATTACATTAGACTTCGATACGCTACAAATGGTGGCTGGAAATACTCTTCCTAATATATCT	1890
Db	561	TyrTyrIleArgLeuArgTyrAlaThrAsnGlyAlaGlyAsnThrLeuProAsnIleSer	580
Qy	1891	CTTACAAATACCGAGTAAATAGGAATACCACTCAACGACTCAACAACACTTTTCTGGT	1950
Db	581	LeuThrIleProGlyValIleGlyIleProProGlnArgLeuAsnAsnThrPheSerGly	600
Qy	1951	ACAAATTTATAATTAATTTACAATACGGAGATTTTGGGTATTTTCCAAATTTCCAAGTACAGTA	2010
Db	601	ThrAsnTyrAsnAsnLeuGlnTyrGlyAspPheGlyTy:PheGlnPheProSerThrVal	620
Qy	2011	ACATTACCTTTAAATCGAAACATACCAATTATTTAATTCGTCGACATGTATCAAAATCA	2070
Db	621	ThrLeuProLeuAsnArgAsnIleProPheIlePheAsnArgAlaAspValSerAsnSer	640
Qy	2071	ATTTTAATCATTCATAAAATTGAATTTATACCAATTTACTTCTCTGTACGCCAAAATAGA	2130
Db	641	IleLeuIleIleAspLysIleGluPheIleProIleThrSerSerValArgGlnAsnArg	660
Qy	2131	GAATAACAAAATTAGAAACTATCCAAACAAAATAATATACATTTTTCACAAATCATACA	2190
Db	661	GluLysGlnLysLeuGluThrIleGlnThrLysIleAsnThrPhePheThrAsnHisThr	680
Qy	2191	AAAAATCTTTAAATATAGAGCCACAAACTATGATATTGAT	2232
Db	681	LysAsnThrLeuAsnIleGluAlaThrAsnTyrAspIleAsp	694
RESULT 3			
ADR89395			
ID	ADR89395 standard; protein; 735 AA.		
AC	ADR89395;		
DT	18-NOV-2004 (first entry)		
DE	AXMI-006.		
KW	delta-endotoxin; delta-endotoxin associate polypeptide;		
KW	expression cassette; transformation; transgenic; plant; bacteria;		
KW	lepidoptera; coleoptera; pest; pesticide; resistance;		
KW	pesticidal activity.		
OS	Bacillus thuringiensis.		
FN	WO2004074462-A2.		
PD	02-SEP-2004.		
PP	20-FEB-2004; 2004WO-US005829.		
XX			

RESULT 3

ADR89395

ID ADR89395 standard: protein: 735 AA:

XX

AC	ADR
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2	2
3	3
4	4
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99	99
100	100

XX

DT 18-NOV-2004 (first entry)

X

**DE AXM**

XX

KW del

KW exp

lept

Bad  
MY  
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XX 55

US 20050100000

WON  
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Ad 20-

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iii







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Db      460 PheIleIleAenGlnIleGluLeuTyrlEuAenGlySerAenAenThrlEuIlystYr 479
Qy      1432 TCAGCTGGGGGAATTTATCTAATGATATAAAACAACTGATTTTCAATTTCTCGTAAAA 1491
Db      480 SerAlaGlyGlySerLeuSerAenTyrlGlnAenThrlPhePheGlnPheProArglys 499
Qy      1492 AAAGACTGTAAACCAATTATTAATCCAAATTTGTTTACCAAGCTATAATAGTATAGTCAT 1551
Db      500 LysAspCyAsAenLeuValIleAspProGlyCySerProAenPheAenAenTyrlSerHis 519
Qy      1552 ATTTTATCCCAAGTTTCTTTATTTAATTTATTCCTATAAAATTTGGATTAGCGCTAAATATA 1611
Db      520 IleLeuSerHisPheSerLeuPheThrlTyrlSerTyrlValIleGlyLeuGlnLeuGlnIle 539
Qy      1612 TTATATACAGGTGCATTTAGGATGGACACACAGTAGTGTATAAGAAATAATGCAATATCA 1671
Db      540 LeuAspThrlGlyValIleGluTyrlTrpThrlHisSerSerValAspArgTyrlAsnAlaIleSer 559
Qy      1672 GATAAAATAATTACAAATGATCCCAAGCAATCAAGGTACACGTCTTGATACAACTCTAAG 1731
Db      560 AspyIleIleThrlMetIleProAlaIleIleGlyAsnAenLeuAspThrlAsnSerIlys 579
Qy      1732 GTAATTGAAGACCTGGTCATACAGGAGAACTTTGGTTTATTTACAAAGTCAAGGGCGT 1791
Db      580 ValIleGluGlyProGlyHisThrlGlyAsnLeuValTyrlLeuGlnSerGlnGlyArg 599
Qy      1792 TTAGAGATTACATGATAGAACTCTTAATTTCTACAAATCTTATTAATACATAGACTCGATAC 1851
Db      600 LeuGluIleThrlCysGluThrlProAenSerThrlGlnSerTyrlPheIleArgLeuArgTyrl 619
Qy      1852 GCTCAAAATGTCGGAAATCTCTCTAATATCTCTTACAAATACCAAGGAGTAAATA 1911
Db      620 AlaThrAenGlyAlaGlyAsnThrlLeuProAenIleSerLeuThrlIleProGlyValIle 639
Qy      1912 GGAATACCACCTCAACGACTCAACAACTTTTCTGCTACAAATTTAATAATTTACAA 1971
Db      640 GlyIleProGlnArgLeuAenAenThrlPheSerGlyThrlAenTyrlAsnAenLeuGln 659
Qy      1972 TACGAGATTTTGGTATTTCCAAATTTCCAAAGTACAGTAACATTAACCTTTAAATCGAAAC 2031
Db      660 TyrlGlyAspPheGlyTyrlPheGlnPheProSerThrlValThrlLeuProLeuAenArgAen 679
Qy      2032 ATACATTTATTTAATTCGTCGAGATGATCAATTCAAATTTAATTTAATTCATTAATTT 2091
Db      680 IleProPheIlePheAenArgAlaAspValSerAenSerIleLeuIleIleAspIysIle 699
Qy      2092 GAATTTATACCAATTTACTTCTCTGTCGCAAAATAGAGAAACAAACAAATTTAGAACT 2151
Db      700 GluPheIleProIleThrlSerSerMetHisGlnAenArgGluIysGlnIysLeuGluThrl 719
Qy      2152 ATCCMAACAAAATAATACATTTTTCACAAATCATACAAA 2193
Db      720 IleGlnThrlYsIleAenThrlPhePheThrlAenHisThrlYs 723

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## RESULT 4

AAP93715

ID AAP93715 standard; protein; 1180 AA.

AC AAP93715;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 30-MAY-1990 (first entry)

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XX      28-DEC-1988.
PD
XX      24-JUN-1988; 88EP-00305772.
PF
XX      26-JUN-1987; 87US-00067653.
PR
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
PA
XX      Ellar DJ, Ward ES;
PI
XX      WPI; 1989-001322/01.
DR
XX      N-PSDB; AAN93059.
XX
PT      DNA fragment encoding insecticidal protein - obtd. from Bacillus
PT      thuringiensis sub species israelensis, and used in microorganisms and
PT      plant cells.
XX
PS      Disclosure; Page; 26pp; English.
XX
CC      The 130 kDa delta-endotoxin from B. thuringiensis subsp. israelensis is
CC      encoded by a 4.46 kb insert of pCH130. The protein is insecticidal and
CC      can be used to control insect pests esp. mosquitos. See also AAP94035.
CC      (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to
CC      correct OS field.)
XX
SQ      Sequence 1180 AA;
Alignment Scores:
Pred. No.: 1.14e-88 Length: 1180
Score: 1159.00 Matches: 283
Percent Similarity: 54.55% Conservative: 131
Best Local Similarity: 37.29% Mismatches: 281
Query Match: 29.42% Indels: 64
DB: Gaps: 25
US-10-782-570-1 (1-2235) x AAP93715 (1-1180)
Qy      13 ANTAATAATGAATGATGATTATCGATTCA-----AAGAAATTTATCTTATCTCTTAAC 66
Db      6 AsnLysAenGluTyrlGluThrlLeuAenAlaSerGlnIlySerLeuAenIleSerAenAen 25
Qy      67 AGAAATATTGATCATCTAGATACCTTACACAAATATCCAAATCAACCAATCAACCAAAAC 126
Db      26 -----TyrThrArgTyrlProIleGluAenSerProIysGlnLeuGlnSer 41
Qy      127 ACAATTAACAAGAGTGGCTCAATATGTGTCAAGGGAATACAAATATGGTGAATAATTC 186
Db      42 ThrAenTyrlYsAspTrpLeuAenMetCysGlnGlnAenGlnIlyTyrlGlyGlyAspPhe 61
Qy      187 GAGACATTTCTAGTCTGATACAAATGCTGTCAGATTAGTCAGGTACTATTGTATCCGGT 246
Db      62 GluThrlPheIleAspSer-----GlyGluLeuSerAlaTyrlThrlIleValIleGly 78
Qy      247 ACTCTGTTAGCGGTATAGTGGCTCCTCTATATCCGACCGATAGGAATAATAGGT 306
Db      79 ThrValLeuThrlGlyPheGlyPheThrlThrl-----ProLeuGlyLeu----- 92
Qy      307 GCTATAATAATATCTTTTGTGACCTTAATCACTGTCTTTTGGCCCGGGAGAACAAAGAC 366
Db      93 ---AlaLeuIleGlyPheGlyThrlLeuIleProValLeuPheProAlaGlnAenGlnSer 111
Qy      367 AAACAGTATGGACACAAATTTAATAATGGGAGAAATTTTGTGTGTATACACCGTTAAACA 426
Db      112 AsnThrl---TrpSerAspPheIleThrlGlnThrlYsAenIleIleIlySerGluIleAla 130
Qy      427 GAAGACATAAACAGCTAAAGTTTACAACTTTAGAGAGATTAGACAAATATTAACAAGC 486
Db      131 SerThrlTyrlSerAenAlaAenIlyIleLeuAenArgSerPheAenValIleSerThrl 150
Qy      487 TATAATACAGCATTTAGATGATGGAGAAATTTAAAGAACTACAAAGCTCTCGATTACCA 546
Db      151 TyrHisAenHisLeuIlystThrlTrpGlu-----AenAenProAenProGln 165

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Db ValThrThrThrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284  
 QY ---AATATGAGATGGAGTATATTAATGATTATCGAAGATATGAGTATTACTGTATTA 942  
 Db GlyAsnIleAsnThrPheAsnThrThrLysMetThrThrAlaValLeu 304  
 QY GATACATCGCTCAATCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGA 1002  
 Db AspLeuValAlaLeuPheProAsnThrAspValGlyLysThrProIle----- 320  
 QY ATAGTGGCATTAACACTGAAGTACAGAGAAATTTATACACTGAATAAATTTGAC 1062  
 Db GlyValGlnSerGluLeuThrArgGluIleThrGlnVal---LeuAsnPheGlu 337  
 QY CGTCTTACTTACCTTGAATTCACCCCAATCTCGCTATAATGGAATATAATTTAACAGT 1122  
 Db GluSerProThrLysThrTyrr-----AspPheGlnThrGlnGluAspSerLeuThrArg 355  
 QY TCAGGGCTTAGATATTTTATGATGAACCTTATATTTATACAAAAAATGAACG 1182  
 Db ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheThrGluLysAlaGlnThr 374  
 QY TACGGGAATCGTTAGTGGTATTCGGAATCGTAAATAGATCTTACTTATGCT----- 1233  
 Db ThrProAsnAsnPhePhe---ThrSerHisThrAsnMetPheHisThrThrLeuAspAsn 393  
 QY ACGACAGGACTGAATTTATATATGAGAGAGACAGGTCCACCCACACAAACAACTTTA 1293  
 Db IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413  
 QY ATACCATTTGAATCTCTATAAAGTTCATTTGTAATGTAAGTATAGACAGTACTTCTCC 1353  
 Db GlyLeuAlaThrAsnIleThrPheLeuLeuAsnValIleSerLeuAspAsn 431  
 QY CTTTTCCTACATATCTTTACAAATTAATCAAAATGAACCTTATTTAAATTAATTCACCT 1413  
 Db LysThrLeuAsnAspThrAsnAsnIleSerLysMetAspPheIleThrAsnGlyThr 451  
 QY AGTAAATTAACATATTCAGCTGGGGGAATTTATCTAAATGATATAAAAA 1464  
 Db ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrThrAspValAsn 470  
 QY ACAACTGATTTTCAATTTCTGTAATAAAGACTGTAAACCAATTTATTAATCCAAATGT 1524  
 Db LysAsnIlePheGlyLeuProIleLysProArgGluAsnGlnAlaIleProThrLeu 490  
 QY TTACCACTATAATAGTATAGTATATTTATCCAGTTTCTTTTATTAATATAT--- 1581  
 Db PheProThrThrAspAsnThrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510  
 QY TCTATATAATTTGGATTAGCGTAAATATATATATATATACAGGTGCTAGGATGACA 1638  
 Db AlaThrThrLys-----ThrGlnValThrThrPheAla-----TrpThr 523  
 QY CACAGTAGTGTAAATAGAAATAATGCAATATCAGATAAAATAATATACATGATCCAGCA 1698  
 Db HisSerSerValAspProLysAsnThrIleThrHisLeuThrThrGlnIleProAla 543  
 QY ATCAAAGGTAACAGCTTTGATACAAACTCTAAGGTAATTAAGAGGACCTGGTCATACAGA 1758  
 Db ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563  
 QY GGAACCTGGTTTATTTACAAAGTCAGGGCGTTTATAGATGATACATGATAGAACTCTAAT 1818  
 Db GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581  
 QY TCTACACACTTATTATACATAGCTTCGATCGCTACAAATGGTGGTGAATACTCTT 1878  
 Db PheGlnGlnSerThrPheIleArgIleArgThrAlaSerAsnGlySerAlaAsnThrArg 601  
 QY CCTAATATATCTTTACATACACAGGAGTAATAGGAATACCACTCAACGACTCAACAC 1938  
 Db AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620

QY ACTTTTCTGTACAAATATATAATTAATTAACATACGAGATTTTGGTATTTCCAAATTT 1998  
 Db ThrPheSerGlyThrAspThrThrAsnLeuLysThrLysAspPheGlnThrLeuGluPhe 640  
 QY CCAAGTACAGTAACATTTACCTTTAAATCGAAACATACCATTTATTAATTCGTCGAGAT 2058  
 Db SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660  
 QY GTA---TCAAATTCATTTAAATCATTTGATATAAATTTGAATTTATATACCAATTTCTCTCT 2115  
 Db ValThrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680  
 QY GTACGCCAAATACAGAAACAAATAATAGAAATCTATCCAAACAAATAAATATACATTT 2175  
 Db IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAsnThrPhe 700  
 QY TTCACAAATCATACAAATAATCTTTAAATATAGAACCAAACTATGATATTTGAT 2232  
 Db TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspThrAspIleAsp 719

## RESULT 9

AAR63078  
 ID AAR63078 standard; protein; 1180 AA.

XX AAR63078;

XX 25-MAR-2003 (revised)

DT 12-AUG-1995 (first entry)

XX B.t. toxin PS71M3.

KW Delta-endotoxin; crystal protein; biological control agent; Calliphoridae;  
 KW screw-worm; sheep blowfly; Lucilia; Phormia; Calliphora; insecticide;  
 KW pesticide; B.t.

OS Bacillus thuringiensis.

XX WO9502694-A2.

XX 26-JAN-1995.

XX 13-JUL-1994; 94WO-US007902.

XX 15-JUL-1993; 93US-00093199.

XX (MYCO ) MYCOGEN CORP.

XX Hickie LA, Payne J;

XX WPI, 1995-067338/09.

XX N-PSDB; AAQ81178.

Method for controlling Calliphoridae pests - specifically utilises  
 Bacillus thuringiensis isolates or toxins.

XX Disclosure; Page 36-38; 50pp; English.

CC A library was constructed from *Bacillus thuringiensis* PS71M3 total  
 CC cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in *Escherichia*  
 CC coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This  
 CC was sequenced (AAQ81178). A cured, acrycystalliferous B.t. host carrying  
 CC pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to  
 CC calliphorids. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 1180 AA;

Alignment Scores:			
Pred. No.:	3,64e-88	Length:	1180
Score:	1153.00	Matches:	282
Percent Similarity:	54.41%	Conservative:	131
Best Local Similarity:	37.15%	Mismatches:	282
Query Match:	29.27%	Indels:	64





Db 661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680  
 QY 2116 GTACCCCAATAGCAAAACAAATAGAACTATCCAAACAAATAAATACATTT 2175  
 Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleIleAsnThrPhe 700  
 QY 2176 TTCACAAATCATACAAAAAATCTTTAAATATAGAGCCACAAACTATGATATTGAT 2232  
 Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnInsrGluLeuThrAspTyrAspIleAsp 719  
 RESULT 10  
 AAE26353  
 ID AAE26353 standard; protein; 1109 AA.  
 XX AC AAE26353;  
 XX DT 13-DEC-2002 (first entry)  
 XX DE Bacillus thuringiensis esp. finitimus cry28Aa1 delta-endotoxin.  
 XX KW Delta-endotoxin; cry26Aa1; cry28Aa1; insect-resistant plant; toxin;  
 KW transgenic host cell; insecticide.  
 XX OS Bacillus thuringiensis.  
 XX PN US2002038005-A1.  
 XX PD 28-MAR-2002:  
 XX PF 08-JAN-2001; 2001US-00756526.  
 XX PR 07-JAN-2000; 2000US-0175158P.  
 XX PA (WOJC/) WOJCIECHOWSKA J A.  
 XX PA (LEWI/) LEWITIN E I.  
 XX PA (ZALU/) ZALUNIN I A.  
 XX PA (REVI/) REVINA L P.  
 XX PA (CHES/) CHESTUKHINA G G.  
 XX PI Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;  
 PI Chestukhina GG;  
 PI WPI; 2002-403936/43.  
 DR N-PSDB; AAD43974.  
 XX Novel isolated delta-endotoxin nucleic acid molecules, cry26Aa1 and  
 PT cry28Aa1 isolated from *Bacillus thuringiensis* finitimus, that encodes  
 PT toxin active against insects, useful for controlling insects.  
 XX Claim 1; Page 37-40; 42pp; English.  
 CC The invention relates to isolated delta-endotoxin nucleic acid molecules,  
 CC cry26Aa1 and cry28Aa1 isolated from *Bacillus thuringiensis* finitimus,  
 CC that encode a toxin that is active against insects. The invention is  
 CC useful for producing an insect-resistant plant, by introducing the  
 CC nucleic acid molecule into the plant, where the nucleic acid is  
 CC expressible in the plant in an effective amount to control an insect. The  
 CC invention is useful for producing a toxin that is active against insects  
 CC by obtaining the transgenic host cell and expressing the nucleic acid  
 CC molecule in the host cell, which results in the toxin that is active  
 CC against insects. The toxin is useful for controlling an insect by  
 CC delivering to the insect an effective amount of toxin. The invention is  
 CC useful for controlling insects. The toxin is useful for inhibiting the  
 CC ability of insect pest to survive, grow or reproduce, for limiting insect  
 CC related damage or loss in crop plants, and to prophylactically treat  
 CC insect susceptible areas or plants to confer protection or resistance  
 CC against harmful insects. The present sequence is *Bacillus thuringiensis*  
 CC sep. finitimus cry28Aa1 delta-endotoxin  
 XX Sequence 1109 AA;

Alignment Scores:

Pred. No.: 6,496-67 Length: 1109

Score: 901.00 Matches: 240  
 Percent Similarity: 49.29% Conservative: 106  
 Best Local Similarity: 34.19% Mismatch: 242  
 Query Match: 22.87% Indels: 114  
 DB: 5 Gaps: 27  
 US-10-782-570-1 (1-2235) x AAE26353 (1-1109)  
 QY 199 AGTCCTGATACAAATGCTGCAGTTAGTCAGGTACTATTGTATCGGTACTCTGTAGCC 258  
 Db 28 SerSerAspThrValAlaValValSerAlaGlyIleValValGlyThrIleLeuThr 47  
 QY 259 GGTATAGGTGGCTCCTCTTCTATATCCGACCGATAGGAATAAATAGGTGCTATATAATA 318  
 Db 48 -----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle 60  
 QY 319 TCTTTTGTACCTTAATCATCTGCTTTTGGCCCGGGGAGAGAAAGAC-----AAACAGTA 375  
 Db 61 SerPheGlyThrLeuAlaProValLeuTrpProAspProGluGluAspProLysLysIle 80  
 QY 376 TGGACACAAATTTATAAATGGGAGAAATTTTGTGTATACACCGTTAACAGAAAGCAT 435  
 Db 81 TrpSerGlnPheMetLysHisGlyLysAspLeuLeuAsnGlnThrIleSerThrAlaVal 100  
 QY 436 AAACAGCTAAAGTTACAAACTTTAGAGGATTTAGACAAATATATTAAGAGCTATATAACA 495  
 Db 101 LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrGluArg 120  
 QY 496 GCATTAGATGATGGAGAAATTTAAAGACTACAAAGCTCTCGGATTTACCACCATCATCA 555  
 Db 121 AlaPheAsnAspTrpLysArg-----AsnProSerAla 131  
 QY 556 GCATTACAAACAGCTGCTTCACTTTAAATACGATTTGAGATGTTTCAACATGATTTT 615  
 Db 132 -----AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHisPheAsn 148  
 QY 616 ATTCGAGAAATACCTGCTTCCAACTTAAAGCTTATAAAGCTTACTTACTTATTTAT 675  
 Db 149 ValSerAsnMetProGlnLeuGlnLeuProThrTyrAspThrLeuLeuLeuSerCysTyr 168  
 QY 676 GCGCAAGCTGCTAATTTTCAATTAATTTATTAACAAGGTGCTGAATTTGGCTGATGAA 735  
 Db 169 ThrGluAlaAlaAsnLeuHisLeuAsnLeuHisGlnGlyValGlnPheAlaAspGln 188  
 QY 736 TGGATGACAGATATACATCTCTCAAAATTTGAACCTATGCTGGAAACATCAGATGACTAT 795  
 Db 189 TrpAsnAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr-----Tyr 205  
 QY 796 TATAAATCTTTTAAAGAAATATACCTAAATATAGTAACTATTTGCAAAATACCTATAGA 855  
 Db 206 TyrAspGluLeuLeuValTyrIleGluLysTyrIleAsnTyrCysThrLysThrTyrHis 225  
 QY 856 GAAGGACTAAATAAATCTCGAAACGAACTTAATATGAGATGGAGATATTTAATGATTAAT 915  
 Db 226 LysGlyLeuAsnHisLeuLysGluSerGluLysIleThrTrpAspAlaTyrAsnThrTyr 245  
 QY 916 CGAAGATATATGACTTACTTGTATAGTACTATCGCTCAATTTCTTTTATGATATA 975  
 Db 246 ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyrAspIle 265  
 QY 976 AAGAGATACAAAGATTTCAATAGGAAGATAGGTGCAATTTAAACCTGAACTTCAAGAGAA 1035  
 Db 266 ArgArgPhePro-----ArgGlyValGluLeuLeuLeuThrArgGlu 279  
 QY 1036 ATTTATACAACTGAAATAAATTTTTCACCGCTTACTTACTTACCTTGAATTCACCAATCTC 1095  
 Db 280 ValTyrThrSer-----LeuAspHisLeuThrArgProGly--- 292  
 QY 1096 GCTATATGGAATATATAATTTAACAGCTTCAGGGCTTAGATTTATTTTATGATGAA 1155  
 Db 293 -----LeuPheThrTrpLeuSerAsp 299  
 QY 1156 CTTATATTTTATACAAAAAATGAAACGTACGGGAATCGTTTGTAGTTGTTGCGAATCGT 1215

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Db 300 IlegluLeuTyThrGluSerValAlaGluGlyAspTyLeuSerGlyLe----- 316
QY 1216 AATAGATCTATTGCTACGACGAGAACTGAAAT-----ATATATGGA 1260
Db 317 ---ArgGluSerLysTyThrGlyAsnGlnPhePheThrMetLysAsnIleTyGly 335
QY 1261 GAAAGAACAGGTCCACCCACCAACAAA-----ACTTAATACCAATTT 1302
Db 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
QY 1303 GAATCTCTAATAGTTTCAATGTAAGTATAGACAAAGTAATCTCTCTCTCTCTCT 1362
Db 351 Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyIleAsn 369
QY 1363 AACATATCTTTACAAATTAATCAATTCGAATTTAATAATTAATTCACCTAGTAATAA 1422
Db 370 LysLeuTySerLeuIleGlnLysIle-----ValPheThrThrPheLysAsnAsp 386
QY 1423 TTAACATATTCAGCTGGGGGGAATTTATCTAATGAT-----AAAAAACCAACTGAT 1473
Db 387 AsnGluTyGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrAsn 406
QY 1474 TTTCAATTTCTGTAAAAAAGACGTAAACCAATTTAATCCAAATTTGTTACCAAGC 1533
Db 407 Tyr-----ProAsnAspTyThrGlyGly 413
QY 1534 TATAATAGT-----TATAGTCATATTTATCCAGITTTCTTTTATTAATATTCCTAT 1587
Db 414 SerAsnSerGlnLysPheLysHisAsnLeuSerHisPheProLeuIleHisLysLeu 433
QY 1588 AAAATTGGATTAGCGCTAAATATATATATATATACAGTGCATTAGGATGACACAGTAGT 1647
Db 434 GluPheAlaGluTyPheHisSerIlePhe-----AlaLeuGlyTyrThrHisAsnSer 451
QY 1648 GTTAATAGAAATATGCAATATCATGATAAAATAATTAACAATGATCCCAAGCAATCAAGGT 1707
Db 452 ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla 471
QY 1708 AACAGCTCTTGATCAAACTCTAAGGTAATTAAGGACCTGTCATACAGGAGGAACCTG 1767
Db 472 TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyGlyAspLeu 490
QY 1768 GTTTATTACAAAGTCAAGGGCGTTAGAGATTATCATGATCACTCTCTAATCTTACACAA 1827
Db 491 IlegluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys 507
QY 1828 TCTTATTACATTAGATTCGATACGCTACAATGGTGTGGAAATACTCTCTCTTAATATA 1887
Db 508 LysTyAlaIleSerLeuPheTyAlaAlaAsnAsnAlaIleAlaValSerIleAspVal 527
QY 1888 TCTCTTACATACAGGAGTAATAGGAATACCACTCAACAGCTCAACACACATTTTCT 1947
Db 528 GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer 541
QY 1948 GGTACAAATTAATAAAT-----TTACAATACGGAGATTTTGGGTATTTC 1992
Db 542 ArgLysGlyAsnAsnAsnAsnPheThrIleGlnAspLeuAsnTyLysAspPheGlnTyHis 561
QY 1993 CAATTTCCAGTACAGTAACATTAACCTTTAATCGAAACATACCACTTTATATTTAATCGT 2052
Db 562 ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHisIleHisLeuLysArg 581
QY 2053 GCAGAT-----GTATCAAAATCAATTTAATCATTTGATAAATTAATTAATTAACCAAT 2106
Db 582 GluAspAspTyThrGluGluGlyValIleLeuLeuIleAspLysLeuGluPheLysProIle 601
QY 2107 ACTTCTCTGTAGCGCAAAATAGAGAAAACAAAAATTAGAAAATCTATCCAAACAAAATA 2166
Db 602 AspGluAsnTyThr-----ThrAsnGluMetAsnLeuGluLysAlaLysLysAlaVal 618
QY 2167 AATACATTTTTCACAAATCATACAAAATACTTTAAATATATAGAGGCCAACCAACTATGAT 2226

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Db 619 AsnValLeuPheIleAsnAlaThr---AsnAlaLeuLysMetAspValThrAspTyHis 637
QY 2227 ATTGAT 2232
Db 638 IleAsp 639

RESULT 11
ADF31302
ID ADF31302 standard; protein; 1109 AA.
AC ADF31302;
DT 12-FEB-2004 (first entry)
DE Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.
XX Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control;
KW transgenic plant; insect resistance; insecticide.
XX Bacillus thuringiensis serovar finitimus.
OS US2003150018-A1.
XX 07-AUG-2003.
XX 15-JAN-2003; 2003US-00345020.
XX 07-JAN-2000; 2000US-0175158P.
XX 08-JAN-2001; 2001US-00756526.
XX (WOJC/) WOJCIECHOWSKA J A.
XX (LEWI/) LEWITIN E I.
XX (ZALU/) ZALUNIN I A.
XX (REVI/) REVINA L P.
XX (CHES/) CHESTURKHINA G G.
XX Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;
XX Chestukhina GG;
XX WPI; 2003-897623/82.
XX N-PSDB; ADF31301.
XX New isolated nucleic acid molecule encoding a toxin that is active
XX against insects useful for controlling insect pests or for conferring
XX insect resistance in plants.
XX Claim 22; SEQ ID NO 4; 42pp; English.
XX The present invention relates to the isolation of novel cry26Aa1 and
XX cry28Aa1 delta-endotoxin genes from Bacillus thuringiensis esp.
XX finitimus. The sequences for the delta-endotoxin polypeptides are also
XX disclosed. The invention provides methods for producing the toxins and
XX compositions containing the toxins. The methods and sequences of the
XX invention are useful for controlling insect pests in transgenic plants to
XX confer insect resistance. The present sequence represents the cry28Aa1
XX delta-endotoxin of the invention.
XX Sequence 1109 AA;

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Alignment Scores:
Pred. No.: 6,49e-67 Length: 1109
Score: 901.00 Matches: 240
Percent Similarity: 49.29% Conservative: 106
Best Local Similarity: 34.19% Mismatches: 242
Query Match: 22.87% Indels: 114
DB: 7 Gaps: 27

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US-10-782-570-1 (1-2235) x ADF31302 (1-1109)

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QY 199 AGTCCTGATCAATTCGTCAGGTACTATTGATATCCGCTACTCTGTAGCC 258
Db 28 SerSerAspThrValAlaValSerAlaGlyIleValValGlyThrIleLeuThr 47

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DT 12-FEB-2004 (first entry)  
 XX Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.  
 DE Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control;  
 XX transgenic plant; insect resistance; insecticide.  
 KW Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control;  
 XX transgenic plant; insect resistance; insecticide.  
 OS Bacillus thuringiensis serovar finitimus.  
 XX US2003154510-A1.  
 XX 14-AUG-2003.  
 XX 15-JAN-2003; 2003US-00342821.  
 XX 07-JAN-2000; 2000US-0175158P.  
 PR 08-JAN-2001; 2001US-00756526.  
 XX (WOJC/) WOJCIECHOWSKA J A.  
 PA (LEWI/) LEWITIN E I.  
 PA (ZALU/) ZALUNIN I A.  
 PA (REVI/) REVINA L P.  
 PA (CHES/) CHESTUKHINA G G.  
 XX Woiciechowska JA, Lewitin EI, Zalunin IA, Revina LP;  
 PI Chestukhina GG;  
 PI  
 XX WPI; 2003-897757/82.  
 DR N-PSDB; ADF31306.  
 XX New delta-endotoxin nucleic acid molecules, cry26Aa1 and cry28Aa1, useful  
 PT for controlling insect pests and for conferring insect resistance.  
 XX Claim 22; SEQ ID NO 4; 42pp; English.  
 XX The present invention relates to the isolation of novel cry26Aa1 and  
 CC cry28Aa1 delta-endotoxin genes from Bacillus thuringiensis ssp.  
 CC finitimus. The sequences for the delta-endotoxin polypeptides are also  
 CC disclosed. The invention provides methods for producing the toxins and  
 CC compositions containing the toxins. The methods and sequences of the  
 CC invention are useful for controlling insect pests in transgenic plants to  
 CC confer insect resistance. The present sequence represents the cry28Aa1  
 CC delta-endotoxin of the invention.  
 XX SQ Sequence 1109 AA;

Alignment Scores:  
 Pred. No.: 6,49e-67 Length: 1109  
 Score: 901.00 Matches: 240  
 Percent Similarity: 49.29% Conservative: 106  
 Best Local Similarity: 34.19% Mismatches: 242  
 Query Match: 22.87% Indels: 114  
 DB: 7 Gaps: 27

US-10-782-570-1 (1-2235) x ADF31307 (1-1109)

QY 199 AGTCGTGATACAAATGTCGAGTAGTCGAGTACTATGTATCGGTAAGTCTGTAGCC 258  
 DB 28 SerSerAspThrValAlaValValSerAlaGlyIleValValGlyThrIleLeuThr 47  
 QY 259 GGTATAGTGGGTCACCTCTATATCCGACCGATAGGAATAATAGGTGCTATAATA 318  
 DB 48 -----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle 60  
 QY 319 TCTTTTGGTACCAATCACTGCTCTTTTGGCCCGCGGAGAACAGAC-AAAACAGTA 375  
 DB 61 SerPheGlyThrLeuAlaProValLeuTrpProAspProGluGluAspProLysIle 80  
 QY 376 TGGACACAAATTTAATAATGGAGAAATTTTGTGTATACACCGTTAAACAGAGCAT 435  
 DB 81 TrpSerGlnPheMetLysHisGlyGluAspLeuLeuAsnGlnThrIleSerThrAlaVal 100  
 QY 436 AAACAGCTAAAGTTACAAAC-TTAGNAGGATTTAGACAAATATTACAAAGCTATAATACA 495

DB 101 LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTrpTyGluArg 120  
 QY 496 GCATTAGATGATTGGAGAAAATTAATAAGACTACAAGCTCTCGATTACCAACCATCATCA 555  
 DB 121 AlaPheAsnAspTrpLysArg-----AsnProSerAla 131  
 QY 556 GCATTACACAGCTGCTTGACTCTTTAAATACGATTTGAGAATGTTCAACATGATTTT 615  
 DB 132 -----AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHisPheAsnPhe 148  
 QY 616 ATTCGAGAAATACCTGCTTCCAACTTGAACTTATAAAACGCTATTACTACCTATTAT 675  
 DB 149 ValSerAsnMetProGlnLeuGlnLeuProThrTrpAspThrLeuLeuLeuSerCysTyr 168  
 QY 676 GCGCAAGCTGCTAATTTTCAATTTAATTAACAACAGGTGCTGTAATGGCTGATGAA 735  
 DB 169 ThrGluAlaAlaAsnLeuHisLeuAsnLeuHisGlnGlyValGlnPheAlaAspGln 188  
 QY 736 TGGATCGCAGATATACATCTCTTCAAAATTTGAACCTAATGCTGGAACATCAGACTAT 795  
 DB 189 TrpAsnAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr-----Tyr 205  
 QY 796 TATAAACTTTTAAAGAAATATATACCTTAAATATAGTAACCTATTCTGCAAAATACATAGA 855  
 DB 206 TyrAspGluLeuLeuValTyrIleGluLysTyrIleAsnTyrCysThrLysThrTyrHis 225  
 QY 856 GAAGGACTAAATAAATTCGAAACGAACTAATATAGATGGAGTATATTAATGATAT 915  
 DB 226 LysGlyLeuAsnHisLeuLysGluSerGluLysIleThrTrpAspAlaTyrAsnThrTyr 245  
 QY 916 CGAAGATATATGACTATTACTGTATATAGACTACTACCTCAATTTCTTTTATGATATA 975  
 DB 246 ArgArgGluMetThrLeuIleValLeuAspLeuValAlaThrPheProPheTyrAspIle 265  
 QY 976 AAGAGTACAAAGATTCAATAGGAAGAATAGGTGGCAATTAACCTGAACTTACAAAGAA 1035  
 DB 266 ArgArgPhePro-----ArgGlyValGluLeuGluLeuThrArgGlu 279  
 QY 1036 ATTATATAAATGAAATAAATTTTGACCGTCTTACTTACCTTGAATTTCAACCAATCTC 1095  
 DB 280 ValTyrThrSer-----LeuAspHisLeuThrArgProGly--- 292  
 QY 1096 GCTATAATGGAATATATTAACACGTTACGGCTAGATATTTTCAATTTTATAGTAA 1155  
 DB 293 -----LeuPheThrTrpLeuSerAsp 299  
 QY 1156 CTTATATTTTATACAAAATGAAACGTCAGCGGAATCGTTTAGTTGGTATTGCGAATCGT 1215  
 DB 300 IleGluLeuTyrThrGluSerValAlaGluGlyAspTyrLeuSerGlyIle----- 316  
 QY 1216 AATAGATCTACTTATGCTACGACAGGAACCTGAAAT-----ATATATGGA 1260  
 DB 317 ---ArgGluSerLysTyrTyrThrGlyAsnGlnPhePheThrMetLysAsnIleTyrGly 335  
 QY 1261 GAAGAACAGCTCCACCCACAAACAAA-----ACTTTAATACCATTT 1302  
 DB 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350  
 QY 1303 GAATCCTATAAGTTTCAATTTGTAACGTAGATGACAAAGTAACCTCTACTTCCCTTTTCC 1362  
 DB 351 Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyLeuAsn 369  
 QY 1363 AACATATCTTTTCAATTAATCAAAATGAACTTTTATTTAATAATCACTAGTAGTAATAA 1422  
 DB 370 LysLeuTyrSerLeuIleGlnLysIle-----ValPheThrPheLysAsnAsp 386  
 QY 1423 TTAACATATTCAGCTGGGGGAATTTATCTAATGAT-----AAAAAACCAATCAT 1473  
 DB 387 AsnGluTyrGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrAsn 406  
 QY 1474 TTTCAATTTCTCTGTAATAAAGACTGTAAACCAATATTATTAATCAAAATTTGTTACCAAGC 1533  
 DB 1533





XX Sick AJ;  
 PI  
 CC WPI: 1991-341902/47.  
 DR N-PSDB; AQL4670.  
 XX  
 PT Bacillus thuringiensis genes encoding diptera-active toxins - and  
 XX transformed microbials used to control insects in various environments.  
 PS  
 CC Claim 3; Page 15; 20pp; English.  
 XX  
 CC The sequence was deduced from the DNA sequence obtd. from plasmid  
 CC pMYC1636 which was isolated from a genomic library prepd. from DNA from  
 CC B.t. P871M3 [from B.t. P871M3-69 (NRRL B-1851)]. It is related to the  
 CC cryIVC toxins from B.t. var. israelensis. The protein has a mol. wt. of  
 CC 77 kD. Microorganisms transformed with the DNA may be administered to  
 CC dipteran insects or their environ- ments, the expressed toxins acting as  
 CC an insecticide. See also AAR14373. (Updated on 25-MAR-2003 to correct PA  
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 675 AA;

## Alignment Scores:

Pred. No.: 8,34e-67 Length: 675  
 Score: 899.00 Matches: 251  
 Percent Similarity: 47.96% Conservative: 114  
 Best Local Similarity: 32.98% Mismatches: 268  
 Query Match: 22.82% Indels: 128  
 DB: 2 Gaps: 32

US-10-782-570-1 (1-2235) x AAR14374 (1-675)

QY 13 PATAATATGATATGAGATTATCGATTCAAGAAATTTATCTTCTTCAACAGAAAT 72  
 DB 6 AsnLysAsnGluTyrGluLeuPheAsnAlaProSerAsnGlyPheSerLysSerAsn 25  
 QY 73 APTGATCTATTCAGATACCTTACACAAATATCAAAATCAACACATTACAAACACAAAT 132  
 DB 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43  
 QY 133 TACAAGAGTGGCTCAATATGTCACAGGGAATACACATATGGTGATATTCGAGACA 192  
 DB 44 TyrLysAspTyrLeuAsnValCysGlnAspAsnGlnTyrGlyAsnAsnAlaGlyAsn 63  
 QY 193 TTTGCTAGTGTGATACATCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 252  
 DB 64 PheValSerSerGluThrIleValGlyValSerAlaGlyIleValGlyValGlyThrMet 83  
 QY 253 TTAGCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGAAATATAGTGTCTATA 312  
 DB 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95  
 QY 313 ATAATATCTTTGGTACCTATACCTGCTTTTGGCGCGCGGAGAACACAGACAAACA 372  
 DB 96 IleIleSerPheGlyThrLeuLeuProIlePheTyr-----GlnGlySerAspProAlaAsn 114  
 QY 373 GTATGACACAAATTTATTAATGGGAGAAATTTTGTGTATACACCGTTACAGAA--- 429  
 DB 115 ValTyrGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130  
 QY 430 -----AGCATAAACACAGCTAAAGTTTACAAACTTTAGAGGATTTAGACAAATATTACAA 483  
 DB 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150  
 QY 484 AGCTATPATACGATATTAGATGATGGAGAAATTTAAAGAACTACAGCTCTGGATTA 543  
 DB 151 LysTyrGlnGluPhePheAspLysTyrGluProAlaArg----- 163  
 QY 544 CCACCATCATCAGCATTACACAGCTGCTTGAATCTTTAAATACGATTTGAGATGTT 603  
 DB 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181  
 QY 604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTCAAACTTATAAA 654

DB 182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199  
 QY 655 ACGCTATTACTACCTATTATTCGCGCAAGCTGCTAATTTTCAATTTTAAATTTTATTACACAA 714  
 DB 200 -----LeuProAlaTyrAlaGlnIleAlaThrThrPheLysLeuAsnLeuLeuLysHis 216  
 QY 715 GGTGCTGAATGGCTGATGAATGCAATGCAGATATACATCTCTTCAAAATTCGAACCTAAT 774  
 DB 217 AlaAlaThrTyrTyrAsnIleTyr-----LeuGlnAsnGlnGlyIleAsnProSer 233  
 QY 775 GCTGGAACATCAGATGACTATTATAA---CTTTTAAAGAAATATACCTAAATATAGT 831  
 DB 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253  
 QY 832 AACTATTCTGCAGAAATACCTATAGAGAGSACTAAATAACTTCGAAACGAACTAATATG 891  
 DB 254 AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273  
 QY 892 AGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATATCATC 951  
 DB 274 ThrTyrAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293  
 QY 952 GCTCAATTTTCTTTTATGATATAAAGATACAGATACAAAGATTCATAGGAGAAATAGTGGC 1011  
 DB 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307  
 QY 1012 ATTAAACTGAACTTACAGAGAAATTTATACACTGAAATAAATTTTTCACCGCTTACT 1071  
 DB 308 ValLysSerGluLeuThrArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326  
 QY 1072 TACCTTGAAATTCACCCCAATCTCGCTAATATGAATATAATTTAACAGCTTCAGGGCTT 1131  
 DB 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339  
 QY 1132 AGATTATTTTCATTTTATGAGAACTATATATTTTATACAAAAT- 1176  
 DB 340 ThrLeuPheThrTyrIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359  
 QY 1177 GAAACGTAC-----CGGAATCGTTTGTAGTTGGTATCGGAATCGTAAT 1218  
 DB 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373  
 QY 1219 AGATCTACTTATGCTACGACGAACTGAAATATATATATGAGAGAAAGACAGCT----- 1272  
 DB 374 ---PheThrHisThrAsnAspArgAsnIleIleTyrGlyAlaValHisGlyHisIle 392  
 QY 1273 ---CCACCCACACAAACAACTTTAATACATTTGAATCTCTAT-----AAAGTT 1317  
 DB 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412  
 QY 1318 TCAATTTGTAACGTAGTACAGTAACCTCTACTCCCTCTTCTTCTCAACATATATTACA 1377  
 DB 413 GluIleValArgHisArgGlu-----TyrSerAsp 422  
 QY 1378 ATTAATCAAAATGAACTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1437  
 DB 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441  
 QY 1438 GGGGGGAATTTATCTAATGATATAAACAACACTGATTTTCAATTTCTCTGTAAGAAAGAC 1497  
 DB 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461  
 QY 1498 TGTAACCAATTTATTAATCCAAATTTGTTTACCAGCTATAATAGTATTAGTATGATTTTAA 1557  
 DB 462 TrpLys-----AsnLysGluTyrGlyHisThrLeu 471  
 QY 1558 TCCAGTTTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1617  
 DB 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg 488  
 QY 1618 ACAGGTGCATTAGGTGGACACACAGTAGTGTGTTAATAGAAATATGCAATATACAGATAA 1677



Db 489 ArgValAlaPheSerTyrThrHisThrSerValAlaPheGlnAsnThrIleAspLeuAsp 508  
 QY 1678 ATAATTACATGATCCAGCAATCAAGGTAACTCTTGATACAACTCTTAAGTAATT 1737  
 Db 509 AenIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528  
 QY 1738 GAAGACCTGGTCATACAGGAGAACTTGGTTATTATTTACAAAGTCAAGGGGTTTAGAG 1797  
 Db 529 LysGlyProGlyHisThrGlyLysAspLeuLysIleLeuLysAspSer-----MetAsp 546  
 QY 1798 ATTACATGTAGA---ACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT 1854  
 Db 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566  
 QY 1855 ACAATGGTGGTGAATACTCTTCTAATATATCTCTTACAAATACCAAGGAGTAAATAGGA 1914  
 Db 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581  
 QY 1915 ATACCACCTCAACGACTCAACAACTTTTCTGGTACAAATTATTAAT-----AATTTA 1968  
 Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600  
 QY 1969 CAATACGGAGATTTTGGGTATTCCAAATTTCCAAGTACAGTA----- 2010  
 Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620  
 QY 2011 -----ACNTACCTTTAATCGAAACATACCATTTATTTAAATCGTGCAGATGTA 2061  
 Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635  
 QY 2062 TCAAAATTCAAATTTAATCATGATAAAATTCGAATTTATACCAATTTCTCTCTGTCAGC 2121  
 Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654  
 QY 2122 CAAATAGAGAAACAAATAATGAAACTATCCAAACAAATAATAATATTTTTCACA 2181  
 Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674  
 QY 2182 AAT 2184  
 Db 675 Asn 675  
 RESULT 15  
 ID ADR89431  
 AC ADR89431 standard; protein; 675 AA.  
 AC ADR89431;  
 DT 18-NOV-2004 (first entry)  
 DE cry10Aa.  
 XX  
 KW delta-endotoxin; delta-endotoxin associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant; bacteria;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO2004074462-A2.  
 XX  
 PD 02-SEP-2004.  
 XX  
 PF 20-FEB-2004; 2004WO-US005829.  
 XX  
 PR 20-FEB-2003; 2003US-0448632P.  
 PR 20-FEB-2003; 2003US-0448633P.  
 PR 20-FEB-2003; 2003US-0448797P.  
 PR 20-FEB-2003; 2003US-0448806P.  
 PR 20-FEB-2003; 2003US-0448810P.  
 PR 20-FEB-2003; 2003US-0448812P.  
 PR 19-FEB-2004; 2004US-00781979.  
 PR 19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.  
 PR 19-FEB-2004; 2004US-00782141.  
 PR 19-FEB-2004; 2004US-00782570.  
 XX 19-FEB-2004; 2004US-00783417.  
 PA (ATHE-) ATHENIX CORP.  
 XX  
 FI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
 XX WPI; 2004-635574/61.  
 DR  
 XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.  
 XX  
 PS Example 6; SEQ ID NO 43; 178pp; English.  
 XX

This sequence represents a delta-endotoxin crystal protein. This protein

was included in the scope of the invention as a comparison to the delta-  
 endotoxins of the invention. Some of the delta-endotoxin coding sequences  
 of the invention have alternative start codons, producing more than one  
 protein from a single open reading frame. The nucleic acid sequences of  
 the invention are useful in DNA constructs or expression cassettes for  
 transformation and expression in plants and bacteria. The nucleic acids  
 and corresponding polypeptides are useful for killing lepidopteran or  
 coleopteran pests. Compositions containing the delta-endotoxins of the  
 invention, and methods for their production, are useful for the  
 production of organisms with pesticide resistance, specifically bacteria  
 and plants. These organisms are useful for generating altered or improved  
 delta-endotoxin or delta-endotoxin-associated proteins that have  
 pesticidal activity, or for detecting the presence of delta-endotoxin or  
 delta-endotoxin-associated proteins or nucleic acids in products or  
 organisms.

Sequence 675 AA;

Alignment Scores:  
 Pred. No.: 1.23e-66 Length: 675  
 Score: 897.00 Matches: 251  
 Percent Similarity: 47.96% Conservative: 114  
 Best Local Similarity: 32.98% Mismatches: 268  
 Query Match: 22.77% Indels: 128  
 DB: 8 Gaps: 32

US-10-782-570-1 (1-2235) x ADR89431 (1-675)

QY 13 AATAAATAATGAATATGAGATTATCGATTCAAGAAATTTATCTTATCTCTTCAACAGAAAT 72  
 Db 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25  
 QY 73 ATTGATCATTTCTAGATACCTTTACACAATAATCCAAATCAACATTACAAACACAAAT 132  
 Db 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43  
 QY 133 TACAAAGAGTGGCTCAATATGCTCAGGGAATACACAATATGCTGATATATTTTCGAGACA 192  
 Db 44 TyrIleAspTrpLeuAsnValCysGlnAspGlnGlnTyrGlyAsnAlaGlyAsn 63  
 QY 193 TTTGCTAGTCTGATACAATTTGCTGCAGGTAGTGCAGTACTATTGTATCCGGTACTCTG 252  
 Db 64 PheAlaSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83  
 QY 253 TTAGCCGGTATAGTGGGCTCACTTCTATATCCGGACCGGATAGAAATAATAGGTGCTATA 312  
 Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95  
 QY 313 ATAATATCTTTTGGTACCTTAATCACTGCTTTTGGCCCGGGAGNACAGACAAACA 372  
 Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp---GlnGlySerAspProAlaAsn 114  
 QY 373 GTATGGACACAAATTTATAAATGGGAGAAATTTTGTGTGATACACCGTTAAACAGAA--- 429  
 Db 115 ValTrpGlnAspLeuAsnIleGly-----GlyArgProIleGlnGluIle 130

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QY 430 -----AGCATAAACAGCTAAAGTTCACAACTTTAGAGGATTTAGACAAATATTACAA 483
Db 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150
QY 484 AGCTATAATACAGCATTAGATGATTGGAGAGAAATTAAGAGACTACAAAGCTCTCGGATTA 543
Db 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg ----- 163
QY 544 CCACATCATCAGCATTTACAAACAGCTGCCCTTGACTCTTAATAATACGATTTGAGAAATGTT 603
Db 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle 181
QY 604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAA 654
Db 182 IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr----- 199
QY 655 ACGCTATTACTACCTATTATGCGCAAGCTGCTCAATTTTCATTTAAATTTATTACAAACAA 714
Db 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLysHis 216
QY 715 GGTGCTGAATGGCTGAATGAATGCAATGACATATACATCTTCACAAATTTGAACCTAAT 774
Db 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
QY 775 GCTGGACATCAGATGACTATTATAA---CTTTTAAAGAAATATATACCTAAATATAGT 831
Db 234 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253
QY 832 AACTATTGTCGAAATACCTATAGAGAGAGCTAAATAAATCTCGAAACGAACTTAATATG 891
Db 254 AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273
QY 892 AGATGGAGTATATTAAATGATTCGAAGATATATGACTATTACTGTTATTAGATCTATC 951
Db 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293
QY 952 GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGATAGGTGGC 1011
Db 294 AlaIlePheProAsnTyrAspProGlnLysTyrProIle-----Gly 307
QY 1012 ATTAACACTGAACCTTACAAGAGAAATTTATACAACTGAAATATAATTTTGACCGTCTTACT 1071
Db 308 ValLysSerGluLeuIleArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326
QY 1072 TACCTTGAATTCACCCCAATCTCGCTATAATGGAATATAATTTAAACAGCTTCAGGCTT 1131
Db 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339
QY 1132 AGATTATTTTTCATTTTATAGTGAACCTATATATTTATACAAAAAT----- 1176
Db 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359
QY 1177 GAAACGTAC-----GGGAATCGTTTGGTATTTGGTATTTGCGAATCGTAAT 1218
Db 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla----- 373
QY 1219 AGATCTACTATTGCTACGACAGGAATCGAAATTTATATATGAGAGAAAGAACAGGT----- 1272
Db 374 ---PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392
QY 1273 ---CACCCACAAACAAACTTTATACCATTTGATCTCTAT-----NAAGTT 1317
Db 393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysPheIleAspLysVal 412
QY 1318 TCAATTTGTAACGTAGTACAGCAAGTAACTCTCTACTTCCCTTTTCCCTAAACATATCTTACA 1377
Db 413 GluIleValArgHisArgGlu-----TyrSerAsp 422
QY 1378 ATTAATCAAAATTTGAACTTTATTATTAATAATATTCACCTAGTAATAATAATTAACATATT 1437
Db 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
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QY 1438 GGGGGGAATTTATCTATATGATAAAAAACAACTGAATTTTCAATTTCTCTGTAAAAAAGAC 1497
Db 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461
QY 1498 TGTAAACCAATATTATTAATCCAAATTTGTTTACCAAGCTATATAGTTATAGTCATATTTA 1557
Db 462 TrpLys-----AsnGluGluTyrGlyHisThrLeu 471
QY 1558 TCCAGTTTCTTTTATTTAATTTCTCTATAAAATTCGATTTAGCGCTAAATATATATAT 1617
Db 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg 488
QY 1618 ACAGTGCATTAGGATCGACACACAGTAGTGTGTTAATAAGAAATATATGCAATATCAGATAAA 1677
Db 489 ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508
QY 1678 ATAATTAATGATCCAGCATCCAGATCAAAAGGTAAACAGTCTTGATACAAACTCTCAAGTAA 1737
Db 509 AsnIleThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528
QY 1738 GAAGGACCTGTCATACAGGAGAACTTGCTTTTATTACAAAGTCAAGGCGGTTTAGAC 1797
Db 529 LysGlyProGlyHisThrGlyAspLeuValIleLeuLysAspSer-----MetAsp 546
QY 1798 ATTACATGTAGA---ACTCCTTAATTTCTACACAACTTTTATTATACATTAGACTTCGATC 1854
Db 547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566
QY 1855 ACAATGGTGTGGAAATACCTTCTTAATATATCTCTTAATATATCTTACAAATCAGGAGTATAGGA 1914
Db 567 ThrAsnAla-----ProLysThrThrValPheLeuThrGlyIleAspThr 581
QY 1915 ATACCACCTCAACGACTCAACACACTTTTCTGTACAAATTTAAT-----AATTTA 1968
Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
QY 1969 CAATACGAGATTTTGGGTATTTCCAAATTTCCAAAGTACAGTA----- 2010
Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620
QY 2011 -----ACATTACCTTTTAAATCGAAACATACCATTTATTTAATTCGTCGACATGTA 2061
Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635
QY 2062 TCAATTCATTAATTAATCATTTGATAAAATTCGAATTTATACCAATTTACTTCTCTGTACGC 2121
Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654
QY 2122 CAAAATAGAGAAAAACAAAATTTAGAAACTATCCAAACAAAAAATAAATACATTTTTCACA 2181
Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674
QY 2182 AAT 2184
Db 675 Asn 675
```

Search completed: January 12, 2006, 06:26:26  
Job time : 235.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 12, 2006, 06:16:09 ; Search time 147 Seconds

(without alignments)  
12705.422 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaatcaaaataataa.....caaaactatgatattgattaa 2235

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US10782570/runat\_12012006\_060223\_7574/app\_query.fasta\_1.2375  
-DB=Published Applications AA Main -QFMT=fastan -SUFFIX=rapbm -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10782570\_@CGN\_1\_1\_248\_@runat\_12012006\_060223\_7574  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3902	99.1	744	US-10-782-570-2	Sequence 2, Appli
2	3623	92.0	694	US-10-782-570-4	Sequence 4, Appli
3	3314	84.1	735	US-10-783-417-2	Sequence 2, Appli
4	1158	29.4	1180	US-10-782-141-12	Sequence 12, Appli
5	1158	29.4	1180	US-10-782-096-14	Sequence 14, Appli
6	1158	29.4	1180	US-10-782-570-10	Sequence 10, Appli
7	1158	29.4	1180	US-10-783-417-8	Sequence 8, Appli
8	1158	29.4	1180	US-10-781-979-14	Sequence 14, Appli
9	901	22.9	1109	US-09-756-526A-4	Sequence 4, Appli
10	901	22.9	1109	US-10-345-020-4	Sequence 4, Appli
11	901	22.9	1109	US-10-342-821-4	Sequence 4, Appli
12	897	22.8	675	US-10-782-141-17	Sequence 17, Appli

13	897	22.8	675	4	US-10-782-096-18	Sequence 18, Appli
14	897	22.8	675	4	US-10-782-570-14	Sequence 14, Appli
15	897	22.8	675	5	US-10-783-417-12	Sequence 12, Appli
16	897	22.8	675	5	US-10-781-979-19	Sequence 19, Appli
17	897	22.8	675	5	US-10-926-819-16	Sequence 16, Appli
18	819	20.8	1136	4	US-10-782-141-13	Sequence 13, Appli
19	819	20.8	1136	5	US-10-781-979-15	Sequence 15, Appli
20	819	20.8	1136	5	US-10-929-754-1	Sequence 1, Appli
21	716	18.2	1210	4	US-10-032-717-4	Sequence 4, Appli
22	716	18.2	1210	4	US-10-414-637-4	Sequence 4, Appli
23	716	18.2	1210	4	US-10-606-320-4	Sequence 4, Appli
24	716	18.2	1210	4	US-10-746-914-4	Sequence 4, Appli
25	709	18.0	682	4	US-10-782-096-20	Sequence 20, Appli
26	709	18.0	682	4	US-10-782-570-16	Sequence 16, Appli
27	709	18.0	682	5	US-10-783-417-14	Sequence 14, Appli
28	709	18.0	682	5	US-10-781-979-21	Sequence 21, Appli
29	708.5	18.0	780	6	US-11-018-615-29	Sequence 29, Appli
30	708.5	18.0	1169	6	US-11-018-615-25	Sequence 25, Appli
31	706	17.9	659	4	US-10-614-076-112	Sequence 112, App
32	706	17.9	659	4	US-10-782-096-12	Sequence 12, Appli
33	706	17.9	659	4	US-10-782-570-9	Sequence 9, Appli
34	706	17.9	659	5	US-10-783-417-7	Sequence 7, Appli
35	700	17.8	652	4	US-10-232-665-4	Sequence 4, Appli
36	700	17.8	652	4	US-10-614-076-110	Sequence 110, App
37	699	17.7	1206	4	US-10-032-717-2	Sequence 2, Appli
38	699	17.7	1206	4	US-10-414-637-2	Sequence 2, Appli
39	699	17.7	1206	4	US-10-606-320-2	Sequence 2, Appli
40	699	17.7	1206	4	US-10-746-914-2	Sequence 2, Appli
41	693	17.6	652	4	US-10-232-665-6	Sequence 6, Appli
42	691	17.5	652	4	US-10-232-665-2	Sequence 2, Appli
43	691	17.5	652	4	US-10-614-076-4	Sequence 4, Appli
44	691	17.5	652	4	US-10-614-076-10	Sequence 10, Appli
45	691	17.5	652	4	US-10-614-076-28	Sequence 28, Appli

## ALIGNMENTS

RESULT 1  
US-10-782-570-2  
; Sequence 2, Application US/10782570  
; Publication No. US2004021096SAI  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274144  
; CURRENT APPLICATION NUMBER: US/10/782,570  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,812  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 744  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-570-2

Alignment Scores:  
Pred. No.: 8.2e-314 Length: 744  
Score: 3902.00 Matches: 743  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.87% Mismatches: 0  
Query Match: 99.06% Indels: 0  
DB: 4 Gaps: 0

US-10-782-570-1 (1-2235) x US-10-782-570-2 (1-744)

QY 1 GTGAATCAAAATAATAATAATGATATGAGATTATCGATTCAAGAAATTATCTTATCT 60

Db .....  
1 MetAsnGlnAsnAsnAsnGluTyrGluIleIleAspSerLysAsnLeuSerTyrPro 20  
QY 61 TCTAAACAGAAATATTGATCATTTCTAGATACCCCTTACACAAATAATCCAAATCAACCAATTA 120  
Db .....  
21 SerAsnArgAsnIleAspHisSerArgTyrProTyrThrAsnAsnProAsnGlnProLeu 40  
QY 121 CAAAACACAAATTACAAAGAGTGGCTCAATATGTCTCAAGGGAATACACATATGGTGAT 180  
Db .....  
41 GlnAsnThrAsnTyrLysGluTyrLeuAsnMetCysGlnGlyAsnThrGlnTyrGlyAsp 60  
QY 181 AATTTCGAGACATTTGCTAGTGTCTGATCAATTCATCAATTCGTCAGTGTAGTGCAGGTACTATTGTA 240  
Db .....  
61 AsnPheGluThrPheAlaSerAlaAspThrIleAlaIleValSerAlaGlyThrIleVal 80  
QY 241 TCCGGTACTCTGTAGCCGTATAGTGGCTCACTTCTATATCCGGACCGATAGGAATA 300  
Db .....  
81 SerGlyThrLeuLeuAlaGlyIleGlyGlyLeuThrSerIleSerGlyProIleGlyIle 100  
QY 301 ATAGTGTCTATAATATATCTTTTGGTACCTTAATCACTGTCTTTTGGCCCGCGGGAGAA 360  
Db .....  
101 IleGlyAlaIleIleSerPheGlyThrLeuIleThrValPheTrpProAlaGlyGlu 120  
QY 361 CAAGACAAAACAGTATGACACAAATTTATTAATGAGGAGAAATTTTGTGTGATACACCG 420  
Db .....  
121 GlnAspLysThrValTrpThrGlnPheIleLysMetGlyGluIlePheValAspThrPro 140  
QY 421 TTAACAGAAAGCATAAAAACAGCTAAAGTTACAAACTTTAGAGGATTTAGACAAATATTA 480  
Db .....  
141 LeuThrGluSerIleLysGlnLeuLysLeuGlnThrLeuGluGlyPheArgGlnIleLeu 160  
QY 481 CAAGCTATATACAGCATAGATGATGGAGAAAATTTAAAGACTACAGCTCCTGGGA 540  
Db .....  
161 GlnSerTyrAsnThrAlaLeuAspAspTrpArgLysLeuLysArgLeuGlnAlaProGly 180  
QY 541 TTACCACCATCATCAGCATTAACAACGCTGCTTACTCTTAAATACGATTTGAGAT 600  
Db .....  
181 LeuProProSerSerAlaLeuGlnGlnAlaLeuThrLeuLysIleArgPheGluAsn 200  
QY 601 GTTCACAAATGATTTTATTCGAAATACCTGGTTTCCAACTTGAACCTTATAAACGCTA 660  
Db .....  
201 ValHisAsnAspPheIleArgGluIleProGlyPheGlnLeuGluThrTyrLysThrLeu 220  
QY 661 TTACTACCTATTTATGCCAAGCTGCTAAATTTTCATTTAAATTTATTAACAACAGGTGCT 720  
Db .....  
221 LeuLeuProIleTyrAlaGlnAlaAlaAsnPheHisLeuAsnLeuLeuGlnGlnGlyAla 240  
QY 721 GAATGGCTGATGAATGAATGCAGATATACATCTCTCACAAATTTGAACCTTAATGCTGGA 780  
Db .....  
241 GluLeuAlaAspGluTrpAsnAlaAspIleHisProSerGlnIleGluProAsnAlaGly 260  
QY 781 ACATCAGATGCTATTATAAACTTTTAAAGAAAATATACCTTAAATATAGTAATATTGT 840  
Db .....  
261 ThrSerAspAspTyrTyrLysLeuLeuLysGluAsnIleProLysTyrSerAsnTyrCys 280  
QY 841 CCAATACCTATAGGAAGGACTAAATTAACCTTCGAAACGAACTTAATATGAGATGGAGT 900  
Db .....  
281 AlaAsnThrTyrArgGluGlyLeuAsnLysLeuArgAsnGluProAsnMetArgTrpSer 300  
QY 901 ATATTTAATGATTATCGAAGATATATGATCTATTACTGTATTAGTACTATCGCTCAATTT 960  
Db .....  
301 IlePheAsnAspTyrArgArgTyrMetThrIleThrValLeuAspThrIleAlaGlnPhe 320  
QY 961 TCTTTTATGATATAAAGATACAAAGATTTCAATAGGAAGAAATAGGTGGCATTTAAAACT 1020  
Db .....  
321 SerPheTyrAspIleLysArgTyrLysAspSerIleGlyArgIleGlyGlyIleLysThr 340  
QY 1021 GAACCTACAGAGAAATTTATCAACTCGAAATAAATTTTGACCGCTTACTTACCTTGAA 1080  
Db .....  
341 GluLeuThrArgGluIleTyrThrThrGluIleAsnPheAspArgLeuThrTyrLeuGlu 360  
QY 1081 ATTCAACCAATCTCGCTATATGAATATATTAATTTAACACGCTTCAGGCTTAGATATTATTT 1140  
Db .....

Db .....  
361 IleGlnProAsnLeuAlaIleMetGluTyrAsnLeuThrArgSerGlyLeuArgLeuPhe 380  
QY 1141 TCATTTTTAGATGAACCTTATATTTTATACAAAAAATGAAACGTACGGGAATCGTTAGTT 1200  
Db .....  
381 SerPheLeuAspGluLeuIlePheTyrThrLysAsnGluThrTyrGlyAsnArgLeuVal 400  
QY 1201 GGTATTCGGAATCGTAATAGATCTACTATGCTACGACAGGAAGTAAATATATATATGGA 1260  
Db .....  
401 GlyIleAlaAsnArgAsnArgSerThrTyrAlaThrThrGlyThrGluIleIleTyrGly 420  
QY 1261 GAAAGAACAGCTGCCACCCACAAACAAACTTTAATACCATTTGAACTCTATAAAGTTTCA 1320  
Db .....  
421 GluArgThrGlyProProThrThrLysThrLeuIleProPheGluSerTyrLysValSer 440  
QY 1321 ATTGTAACTGATAGACAAAGTAACCTCTACTTCCCTTTTCTTAAACATATATCTTACAAT 1380  
Db .....  
441 IleValThrAspArgGlnValThrProThrSerProPheProAsnIleTyrPheThrIle 460  
QY 1381 AATCAAAATTGAACCTTATTTAAATAATTCACCTAGTAAATAATTAACATATTCAGCTGGG 1440  
Db .....  
461 AsnGlnIleGluLeuTyrLeuAsnAsnSerProSerAsnLysLeuThrTyrSerAlaGly 480  
QY 1441 GGGAAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCTCTGTAATAAAGACTGT 1500  
Db .....  
481 GlyAsnLeuSerAsnAspLysLysThrThrAspPheGlnPheProValLysLysAspCys 500  
QY 1501 AAACCAATTTAATCCAAATTTGTTTACCAAGCTATATATAGTTATAGTATATTTATCC 1560  
Db .....  
501 LysProIleIleAsnProAsnCysLeuProSerTyrAsnSerTyrSerHisIleLeuSer 520  
QY 1561 CAGTTTCTTTTATTTAATTTCTATATAAATTTGGATTAGGCTTAATATATATATATACA 1620  
Db .....  
521 GlnPheSerLeuPheAsnTyrSerTyrLysIleGlyLeuAlaLeuAsnIleLeuTyrThr 540  
QY 1621 GGTGCATTTAGAGTGGACACACAGTAGTGTAAATAGAAATTAATGCAATATCAGATAAATA 1680  
Db .....  
541 GlyAlaLeuGlyTrpThrHisSerSerValAsnArgAsnAlaIleSerAspLysIle 560  
QY 1681 ATTACAAATGATCCCAAGCAATCAAGGTAAACAGTCTTGATACAACTCTAAGGTAAATGAA 1740  
Db .....  
561 IleThrMetIleProAlaIleLysGlyAsnSerLeuAspThrAsnSerLysValIleGlu 580  
QY 1741 GGACCTGCTATACAGGAGGAACCTGGTTTATTTACAAAGTCAAGGCGCTTAGAGATT 1800  
Db .....  
581 GlyProGlyHisThrGlyGlyAsnLeuValTyrLeuGlnSerGlnGlyArgLeuGluIle 600  
QY 1801 ACATGTAGAATCCTTAATCTACCAATCTTATACATTAAGACTTCGATACGCTACAAAT 1860  
Db .....  
601 ThrCysArgThrProAsnSerThrGlnSerTyrTyrIleArgLeuArgTyrAlaThrAsn 620  
QY 1861 GGTGCTGGAATACTCTTCTTAATATATCTTCAATACATACAGGAGTAATAGGAATACCA 1920  
Db .....  
621 GlyAlaGlyAsnThrLeuProAsnIleSerLeuThrIleProGlyValIleGlyIlePro 640  
QY 1921 CCTCAAGCTACCAACACACTTTTCTGGTACAAATTAATTAATTTACATACGAGAT 1980  
Db .....  
641 ProGlnArgLeuAsnAsnThrPheSerGlyThrAsnTyrAsnAsnLeuGlnTyrGlyAsp 660  
QY 1981 TTTGGGTATTTCCAAATTTCCAAGTACAGTAACATTAACCTTTTAAATCGAAACATACCATTT 2040  
Db .....  
661 PheGlyTyrPheGlnPheProSerThrValThrLeuProLeuAsnArgAsnIleProPhe 680  
QY 2041 ATATTTAATCGTCAGATGTATCAAAATTTCAATTTTATCTTCAATTAATAAATTTGAAATTTATA 2100  
Db .....  
681 IlePheAsnArgAlaAspValSerAsnSerIleLeuIleIleAspLysIleGluPheIle 700  
QY 2101 CCAATTAATCTCTCTGTACCCCAAAATAGAGAAAACAAAAATTAGAACTATCCAAACA 2160  
Db .....  
701 ProIleThrSerSerValArgGlnAsnArgGluLysGlnLysLeuGluThrIleGlnThr 720  
QY 2161 AAAATAAATACATTTTTCACAAATCATACAAAAAATCTTTAAATATAGAGCCACAAAC 2220  
Db .....  
721 LysIleAsnThrPhePheThrAsnHisThrLysAsnThrLeuAsnIleGluAlaThrAsn 740

QY 2221 TATGATATTGAT 2232  
| | | | | | | | | |  
Db 741 TyrAspIleAsp 744  
| | | | | | | | | |  
RESULT 2  
US-10-782-570-4  
; Sequence 4, Application US/10782570  
; Publication No. US20040210965A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274144  
; CURRENT APPLICATION NUMBER: US/10/782,570  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,812  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 694  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-570-4

Alignment Scores:  
Pred. No.: 9 58e-291 Length: 694  
Score: 3623.00 Matches: 694  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 91.98% Indels: 0  
DB: 4 Gaps: 0

US-10-782-570-1 (1-2235) x US-10-782-570-4 (1-694)

QY 151 ATGTCGAAGGAATACAAATATGGTGAATAATTCGAGACATTTGCTAGTCTGATACA 210  
| | | | | | | | | |  
Db 1 MetCysGlnGlyAsnThrGlnTyrGlyAspAsnPheGluThrPheAlaSerAlaAspThr 20  
| | | | | | | | | |  
QY 211 ATGTCGAGTTAGTCAGGACTATTGTCCTGCTCTCTGTTAGCCGGTATAGTGG 270  
| | | | | | | | | |  
Db 21 IleAlaAlaValSerAlaGlyThrIleValSerGlyThrLeuLeuAlaGlyIleGlyGly 40  
| | | | | | | | | |  
QY 271 CTCACCTCTATATCCGACCGCATAGGAATAATAGGTGCTATATAATATCTTTGGTACC 330  
| | | | | | | | | |  
Db 41 LeuThrSerIleSerGlyProIleGlyIleGlyAlaIleIleIleSerPheGlyThr 60  
| | | | | | | | | |  
QY 331 CTAATCAGTCTTTTGGCCCGGAGAACAGACAAACAGTATGGACACAAATTTAT 390  
| | | | | | | | | |  
Db 61 LeuIleThrValPheThrProAlaGlyGluGlnAspLysThrValTrpThrGlnPheIle 80  
| | | | | | | | | |  
QY 391 AAAATGGGAGAAATTTTGTTCATACACCGTTAAACAGAACATAAACAGCTAAAGTTA 450  
| | | | | | | | | |  
Db 81 LysMetGlyGluIlePheValAspThrProLeuThrGluSerIleIleGlnLeuLysLeu 100  
| | | | | | | | | |  
QY 451 CAAACTTTAGAGGATTATAGACAAATATTAACAAAGCTATAATACAGCATTAGATGG 510  
| | | | | | | | | |  
Db 101 GlnThrLeuGluGlyPheArgGlnIleLeuGlnSerTyrAsnThrAlaLeuAspThr 120  
| | | | | | | | | |  
QY 511 AGAAATTTAAAGACTACAGCTCTCGATTACCAACCATCATCAGCATTACACAAGCT 570  
| | | | | | | | | |  
Db 121 ArgLysLeuLysArgLeuGlnAlaProGlyLeuProProSerSerAlaLeuGlnAla 140  
| | | | | | | | | |  
QY 571 GCCTTCAGCTTTAAATACAGATTGAGATGTTTCAATGATTTTATTCAGAAATACCT 630  
| | | | | | | | | |  
Db 141 AlaLeuThrLeuLysIleArgPheGluAsnValHisAsnAspPheIleArgGluIlePro 160  
| | | | | | | | | |  
QY 631 GGTTCCTCAACTTATAAACCGCTATTACTACTATTATTTATGCGCAAGCTGCTAAT 690  
| | | | | | | | | |

Db GlyPheGlnLeuGluThrTyrLysThrLeuLeuLeuProIleTyrAlaGlnAlaAlaAsn 180  
| | | | | | | | | |  
QY 691 TTTTCATTTAAATTTATTACAAAGGTGCTGAATTTGGCTGATGAATGAATGAATGAATGA 750  
| | | | | | | | | |  
Db 181 PheHisLeuAsnLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 200  
| | | | | | | | | |  
QY 751 CATCTTTCACAAATTTGAACCTTAATGCTGGAAACATCAGATGACTATTATAAACTTTTAAA 810  
| | | | | | | | | |  
Db 201 HisProSerGlnIleGluProAsnAlaGlyThrSerAspAspTyrTyrLysLeuLeuLys 220  
| | | | | | | | | |  
QY 811 GAAATATACCTAATATATAGTAATCTATTGTCGCAATACCTATAGAGAAGGACTAAATAAA 870  
| | | | | | | | | |  
Db 221 GluAsnIleProLysTyrSerAsnTyrCysAlaAsnThrTyrArgGluGlyLeuAsnLys 240  
| | | | | | | | | |  
QY 871 CTTCGAAACGAACCTAATATGAGATGAGTATATTATGATGATATCGAAGATATATGACT 930  
| | | | | | | | | |  
Db 241 LeuArgAsnGluProAsnMetArgTrpSerIlePheAsnAspTyrArgArgTyrMetThr 260  
| | | | | | | | | |  
QY 931 ATTACTGTATTAGATACCTATCGCTCAATTTTCTTTTATGATATATAAGAGATACAAAGAT 990  
| | | | | | | | | |  
Db 261 IleThrValLeuAspThrIleAlaGlnPheSerPheTyrAspIleLysArgTyrLysAsp 280  
| | | | | | | | | |  
QY 991 TCAATAGGAAGAAATAGGTGGCAATTAAACTGAACTTACAAGAGAAATTTATACAACGAA 1050  
| | | | | | | | | |  
Db 281 SerIleGlyArgIleGlyIleLysThrGluLeuThrArgGluIleTyrThrThrGlu 300  
| | | | | | | | | |  
QY 1051 ATAAATTTTGACCTCTTACTTACCTTGAAATTCACACCAATCTCGCTATATATGCAATAT 1110  
| | | | | | | | | |  
Db 301 IleAsnPheAspArgLeuThrTyrLeuGluIleGlnProAsnLeuAlaIleMetGluTyr 320  
| | | | | | | | | |  
QY 1111 AATTTAACACCTTCAGGGCTTAGATATTATTTCAATTTTATGATGAACTTATTTTATACA 1170  
| | | | | | | | | |  
Db 321 AsnLeuThrArgSerGlyLeuArgLeuPheSerPheLeuAspGluLeuIlePheTyrThr 340  
| | | | | | | | | |  
QY 1171 AAAAATGAAACGTACGGGAATCGTTTACTGCTATGCGAATCGAATCGAATGATCTACTTAT 1230  
| | | | | | | | | |  
Db 341 LysAsnGluThrTyrGlyAsnArgLeuValGlyIleAlaAsnArgAsnArgSerThrTyr 360  
| | | | | | | | | |  
QY 1231 GCTACGACAGAACTGAATTTATATATGAGAAAGAAACAGGTCCACCCACCAACAAACT 1290  
| | | | | | | | | |  
Db 361 AlaThrThrGlyThrGluIleIleTyrGlyGluArgThrGlyProProThrThrLysThr 380  
| | | | | | | | | |  
QY 1291 TTAATACCATTTGAATCTCTATAAAGTTTCAATTTGTAACGTAGACAAAGTAACTCTACT 1350  
| | | | | | | | | |  
Db 381 LeuIleProPheGluSerTyrLysValSerIleValThrAspArgGlnValThrProThr 400  
| | | | | | | | | |  
QY 1351 TCCCTTTTCTTAACATATCTTTACAATTAATCAAAATGAACTTTTATTAATTAATTCAC 1410  
| | | | | | | | | |  
Db 401 SerProPheProAsnIleTyrPheThrIleAsnGlnIleGluLeuTyrLeuAsnAsnSer 420  
| | | | | | | | | |  
QY 1411 CCTAGTAATAATTAACATATTTACGCTGGGGGAATTTATCTAATGATAAAAAACAACCT 1470  
| | | | | | | | | |  
Db 421 ProSerAsnLysLeuThrTyrSerAlaGlyAsnLeuSerAsnAspLysLysThrThr 440  
| | | | | | | | | |  
QY 1471 CATTTTCAATTTCTGTAAAAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCA 1530  
| | | | | | | | | |  
Db 441 AspPheGlnPheProValLysLysAspCysLysProIleIleAsnProAsnCysLeuPro 460  
| | | | | | | | | |  
QY 1531 AGCTATAATAGTTATAGTCATATTTTATCCAGTCTTTTCTTTTATTAATTTTCTCTATAAA 1590  
| | | | | | | | | |  
Db 461 SerTyrAsnSerTyrSerHisIleLeuSerGlnPheSerLeuPheAsnTyrSerTyrLys 480  
| | | | | | | | | |  
QY 1591 ATTGATTAGCGCTAAATATATATATACAGTGCATTTAGGATGACACACAGTAGTGT 1650  
| | | | | | | | | |  
Db 481 IleGlyLeuAlaLeuAsnIleLeuTyrThrGlyAlaLeuGlyTyrThrHisSerSerVal 500  
| | | | | | | | | |  
QY 1651 AATGAAATTAATGCAATATCAGATAAAATAATTAATGATGATCCAGCAATCAAAGGTAC 1710  
| | | | | | | | | |  
Db 501 AsnArgAsnAsnAlaIleSerAspLysIleIleThrMetIleProAlaIleLysGlyAsn 520  
| | | | | | | | | |  
QY 1711 AGTCTTGATACAACTCTAAGGTAATGAAGCACTGCTGTCATACAGGAGAACTTGTT 1770  
| | | | | | | | | |

```
Db 521 SerLeuAspThrAsnSerLysValIleGluGlyProGlyHisThrGlyGlyAsnLeuVal 540
QY 1771 TATTACAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCCTAAATCTTACACAACTCT 1830
Db 541 TyrLeuGlnSerGlnGlyArgLeuGluIleThrCysArgThrProAsnSerThrGlnSer 560
QY 1831 TATTACATTAGACTTCGATACCTCAATCAATGGTGTGGAAATACCTCTTCCCTAATATATCT 1890
Db 561 TyrTyrIleArgLeuArgTyrAlaThrAsnGlyAlaGlyAsnThrLeuProAsnIleSer 580
QY 1891 CTTCAATACCAAGGAGTAAATAGGATACCACTCAACGACTCAACAAACACTTTTCTGGT 1950
Db 581 LeuThrIleProGlyValIleGlyIleProGlnArgLeuAsnAsnThrPheSerGly 600
QY 1951 ACAAAATATAAATTAACAATCCGAGATTTGGGTATTTCCCAATTTCCCAAGTACAGTA 2010
Db 601 ThrAsnTyrAsnAsnLeuGlnTyrGlyAspPheGlyTyrPheGlnPheProSerThrVal 620
QY 2011 ACATTACCTTTAAATCGAAACATACCTATTTATTTAATCGTGCAGATGTATCAAAATCA 2070
Db 621 ThrLeuProLeuAsnArgAsnIleProPheIlePheAsnArgAlaAspValSerAsnSer 640
QY 2071 ATTTTAATCATTGATAAAATGAAATTTATATACCAATTTACTTCTCTGTAGCGCAAAATAGA 2130
Db 641 IleLeuIleIleAspLysIleGluPheIleProIleThrSerSerValArgGlnAsnArg 660
QY 2131 GAAAAACAAAATTAAGAACTATCCAAACAAAATAAATACATTTTCCAAAAATCATACA 2190
Db 661 GluLysGlnLysLeuGluThrIleGlnThrLysIleAsnThrPhePheThrAsnHisThr 680
QY 2191 AAAAATACCTTTAAATPATAGAGCCCAAACTATGATATTGAT 2232
Db 681 LysAsnThrLeuAsnIleGluAlaThrAsnTyrAspIleAsp 694
```

## RESULT 3

```
US-10-783-417-2
; Sequence 2, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10/783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-783-417-2
```

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Alignment Scores:
Pred. No.: 3,49e-265 Length: 735
Score: 3314.00 Matches: 638
Percent Similarity: 91.28% Conservative: 32
Best Local Similarity: 86.92% Mismatches: 60
Query Match: 84.13% Indels: 4
DB: 5 Gaps: 3
```

US-10-782-570-1 (1-2235) x US-10-783-417-2 (1-735).

```
QY 1 GTGAATCAAATAAT---AATAAGATATAGAGATTATCGATTCAAGAAATTTATCTTAT 57
Db 1 MetAsnGlnAsnAsnAspAsnAsnGluTyrGluIleIleAspSerHisThrSerProTyr 20
```

```
QY 58 CTTTCTAACAGAAATATTGATCATTTCTAGATACCCCTTACACAAATAATCCAAATCAACCA 117
Db 21 PheProAsnArgAsnSerAsnAspSerArgTyrProTyrThrAsnAsnProAsnGlnPro 40
QY 118 TTACAAAACACAAATTAACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT 177
Db 41 LeuGlnAsnThrAsnTyrLysGluTyrLeuAsnMetCysGlnGlyAsnThrGlnTyrGly 60
QY 178 GATAATTTCCAGACATTTGCTAGTGTGATACAAATCTGCAGTGTAGTGGAGGTACTATT 237
Db 61 AspAsnPheGluThrPheAlaSerAlaAspThrIleAlaAlaValSerAlaGlyThrIle 80
QY 238 GTATCCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATATCCGACCCATAGGA 297
Db 81 ValSerGlyThrLeuLeuAlaGlyIleGlyGlyLeuThrSerIleSerGlyProIleGly 100
QY 298 ATAATAGGTCTATAATAATATCTTTTGGTACCTAATCACTGTCTTTTGGCCCGCGGA 357
Db 101 IleIleGlyAlaIleIleIleSerPheGlyThrLeuIleThrValPheTyrProAlaGly 120
QY 358 GAACAGACAAAACAGCTATCGACACAATTTTAAATGGAGAAAATTTTGTGTATACA 417
Db 121 GluGlnAspLysThrValTyrThrGlnPheIleLysMetGlyGluIlePheValAspThr 140
QY 418 CCGTTAACAGAAAGCAATAACAGCTAAAGTTACAACTTTAGAGGATTTAGACAATA 477
Db 141 ProLeuThrGluSerIleLysGlnLeuLysLeuGlnThrLeuGluGlyPheArgGlnIle 160
QY 478 TTACAAAGCTATTAATACAGCATTTAGATGATTTGGAGAAAATTTAAAAAGACTCAAGCTCCT 537
Db 161 LeuGlnSerTyrAsnThrAlaLeuAspAspTyrArgLysLeuLysArgLeuGlnAlaPro 180
QY 538 GGATTACCACCATCATCAGCATTTACACAAGCTGCCTTGACTCTTAAATAATACGATTGAG 597
Db 181 GlyLeuProProSerSerAlaLeuGlnGlnAlaAlaLeuThrLeuLysIleLeuGlu 200
QY 598 AATGTTCAACAATGATTTTTCGAGAAATACCTGGTTCCCACTTCAAACTTATAAAACG 657
Db 201 AsnValHisAsnAspPheIleArgGluIleProGlyPheGlnLeuGluThrTyrLysThr 220
QY 658 CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTAAATTTATTACAAAGGT 717
Db 221 LeuLeuLeuProIleTyrAlaGlnAlaAlaAsnPheHisLeuAsnLeuLeuGlnGly 240
QY 718 GCTGAATTTGGCTGATGAATGGAATGCAGATATACATCCTTCAACAATTTGAACCTATGCT 777
Db 241 AlaGluLeuAlaAspGluTyrAsnAlaAspIleHisProSerGlnIleGluProAsnAla 260
QY 778 GGAACATCAGATGACTATTATAAACTTTTAAAGAAAATATACCTAAATATAGTAACTAT 837
Db 261 GlyThrSerAspAspTyrTyrLysLeuLeuLysGluAsnIleProLysTyrSerAsnTyr 280
QY 838 TGTGCAAAATACCTATAGAGAGACTATAAATAAATCTTCAAAACGAACCTAATATGAGATGG 897
Db 281 CysAlaAsnThrTyrArgThrGlyLeuLysAsnLeuArgAspGluProAsnMetLysTyr 300
QY 898 AGTATATTTAATGATTTATCGAAGATATATGACTATTTACTGTATATAGTACTATCGCTCAA 957
Db 301 SerIlePheAsnAspTyrArgArgTyrMetThrIleThrValLeuAspThrIleSerGln 320
QY 958 TTTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGA-----AGAATAGGTGGC 1011
Db 321 PheSerLeuTyrAspIleLysArgTyrArgAspSerIleGlyGlyIleGluValLysGly 340
QY 1012 ATTAATAACTGAACCTTACAAGAGAAAATTTATACAACCTGAAATAAATTTTGCACCGCTTACT 1071
Db 341 IleLysAsnGluLeuThrArgGluIleTyrThrThrGluIleAsnPheAspArgLeuPro 360
QY 1072 TACCTTGAATTCACCCCAATCTCGCTATATATGGAATATAATTTAAACAGTTCAGGGCTT 1131
Db 361 GlnLeuArgValGlnProAsnLeuAlaThrMetGluTyrAsnLeuThrArgAlaSerPhe 380
QY 1132 AGATTATTTTTCATTTTAGATGACTTATATTTTATACAAAAAATGAAACGTACGGGAAT 1191
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```

; Sequence 12, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-12

Alignment Scores:
Pred. No.: 7,86e-87 Length: 1180
Score: 1158.00 Matches: 283
Percent Similarity: 54.55% Conservative: 131
Best Local Similarity: 37.29% Mismatches: 281
Query Match: 29.40% Indels: 64
DB: 4 Gaps: 25

US-10-782-570-1 (1-2235) x US-10-782-141-12 (1-1180)
QY 13 AATAATGAATGATGAGATTATCGATTCA-----AAGAAATTTATCTTATCTCTCTAAC 66
DB 6 AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
QY 67 AGAAATATGATCATCTTAGATACCTTTACACAATAATCCAAATCAACCACTTACAAAAC 126
DB 26 -----TyrThrArgTyrProIleGluAsnSerProLysGlnLeuLeuGlnSer 41
QY 127 ACAATTAACAAGAGTGGCTCAATATATGTGTCAAGGGAATACACAATATGGTGAATATTC 186
DB 42 ThrAsnTyrLysAspTyrLeuAsnMetCysGlnGlnAsnGlnTyrGlyGlyAspPhe 61
QY 187 GAGACATTTGCTAGTGTGATACAAATTCCTGCGAGTAGTGCAGGTACTATTGTCCTCGT 246
DB 62 GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValValGly 78
QY 247 ACTCTGTTAGCGGTATAGTGGGTCTACTTCTATATCCGGACCGATAGGAATAATAGT 306
DB 79 ThrValLeuThrGlyPheGlyPheThrThr-----ProLeuGlyLeu----- 92
QY 307 GCTATAATAATATCTTTTGGTACCTAATCACTGTCTTTTGGCCCGCGGAGAACAGAC 366
DB 93 ---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111
QY 367 AAAACAGTATGACACAATAATTTATAAATGGGAGAAATTTTGTGTGATACACCGTTAAC 426
DB 112 AsnThr---TyrSerAspPheIleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
QY 427 GAAAGCAATAAACAGCTAAAGTTACAACTTTAGNAGGATTTAGACAATATTACAAAGC 486
DB 131 SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150
QY 487 TATAATACAGCATTAGATGATTGGAGAAAATTTAAAGACTACAAAGCTCCTCGATTACCA 546
DB 151 TyrHisAsnHisLeuLysThrTyrGlu-----AsnAsnProAsnProGln 165
QY 547 CCATCATCAGCATTAACAAGAGCTGCTTGTAGTCTTTAAATACGATTTGAGATGTTTAC 606
DB 166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
```

RESULT 4

US-10-782-141-12



```
QY 607 AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACCTTGAACCTTATAAAACGCTA 660
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
186 ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrThrAsnIleLeu 205
QY 661 TTACTACCTATTATTCGCAAGCTGCTAATTTTCAATTTTAAATTTATTACAACAGGTGCT 720
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
206 ValLeuSerSerTyrAlaGlnAlaAsnLeuHleLeuThrValLeuAsnGlnAlaVal 225
QY 721 GAATGGCTGATGAATGGATCGAGATATACATATACCTCTCAAAATTTGAACCTTAATCCTGA 780
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
226 LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro----LeuPro 244
QY 781 ACATCAGATGACTATTATAAATCTTTTAAAGAGAAATATATACCTTAAATATAGTAACCTATTGT 840
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
245 ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnIleCys 264
QY 841 GCAATATCTATAGAGAGGACTAATAAATCTTGAAGACGAACCT-----885
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
265 ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrProAspSerAsnLeuAsp 284
QY 886 ---AATATCAGATCGAGTATATTTAATGATTCGAGATATATACCTACTACTGTATTA 942
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
285 GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrAlaValLeu 304
QY 943 GATACCTATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAAGA 1002
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
305 AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle-----320
QY 1003 ATAGTGGCAATTAACCTGAACCTTACAAGAGAAATTTATACAACTGAAATTAATTTTGAC 1062
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
321 ----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal--LeuAsnPheGlu 337
QY 1063 CGTCTTACTTACTTGAATTCACCCCAATCTCGCTATTAATGGAATATAATTTAACAGT 1122
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
QY 1123 TCAGGGCTTAGATATTTTCATTTTAGATGAACCTTATATTTATACAAAAAATGAAACG 1182
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
QY 1183 TACGGGAATCGTTTATGTTATTCGAATCGTAAATAGATCTACTTTATGCT-----1233
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
QY 1234 ACACAGCAAGCACTGAATTTATATATCGAGAGAAACAGGTCCACCACCAACAAACTTTA 1293
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
QY 1294 ATACCAATTTGAATCTATAGAGTTTCAATTTGTAACGTAGACAAAGTAACTCTACTTCC 1353
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
414 -----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn 431
QY 1354 CTTTTCCTTAACATATCTTTTACAATTAATCAAATTTGAACCTTTTAAATTAATTTACCT 1413
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451
QY 1414 -----AGTAATAATTAACATATTCAGCTGGGGGAATTTATCTAAATGATATAAAAA 1464
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
452 ArgLeuLeuGluLysLeuThr---AlaGlySerGlyGlnIleTyrTrpAspValAsn 470
QY 1465 ACNACTGATTTTCAATTTTCTGTAATAAAAGACTGTAAACCAATTTATTAATCCAAATGT 1524
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
471 LysAsnIlePheGlyLeuProIleLeuLysArgArgGluAsnGlnGlyAsnProThrLeu 490
QY 1525 TTACAAGCTATAATAGTATAGTCATATTTATCCAGTTTCTCTTTATTTAAATAT---1581
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510
QY 1582 ---TCTTATAAATTTGGATTACCGCTAAATATATATATATATACAGGTGCATAGGATGACA 1638
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TrpThr 523
QY 1639 CACAGTAGTGTAAATAGAAATAATGCAATATCAGATATAAATAATTTACAATGATCCAGCA 1698
```

```
Db 524 HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProIla 543
QY 1699 ATCAAAGGTAACTCTTGATACAAACTCTAAGGTAATTAAGGACCTGGTCATACAGGA 1758
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
544 ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563
QY 1759 GGAACCTTGGTTTATTACAAAGTCAAGGGCGTTTACAGATTACATGTAGAACCTCCTAAT 1818
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
QY 1819 TCTACACATCTTATTACATTTAGACTTCGATACCTACAAATGTGTCTGGAAATACTCTT 1878
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
582 PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601
QY 1879 CCTAATATATCTTCAATACACAGGAGTAAATAGAAATACCACTCAACGACTCAACAAC 1938
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620
QY 1939 ACTTTTCTGTCGTAACAATTAATAATTTACAATACGAGATTTTGGGTATTTCCAATTT 1998
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640
QY 1999 CCAAGTACAGTAACATTTACCTTTAAATCGAAACATACCATTTATATATTAATCGTCAGAT 2058
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
QY 2059 GTA---TCAAATTCATTTTAATCATTTGATAAATTAATTAATTAATTAATTAATTAAT 2115
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
QY 2116 GTAGCCAAATAGAGAAAAACAAAATTTAGAACTATCCAAACAAAATTAATTAATTAAT 2175
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAsnThrPhe 700
QY 2176 TTCCAATCATACAAAAATCTTTAAATATAGAACCCACAACTATGATATTGAT 2232
Db   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

RESULT 5
US-10-782-096-14
; Sequence 14, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-14

Alignment Scores:
Pred. No.: 7,86e-87 Length: 1180
Score: 1158.00 Matches: 283
Percent Similarity: 54.55% Conservativeness: 131
Best Local Similarity: 37.29% Mismatches: 281
Query Match: 29,40% Indels: 64
DB: 4 Gaps: 25

US-10-782-570-1 (1-2235) x US-10-782-096-14 (1-1180)
```



```

Db 681 ileArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleLeuAsnThrPhe 700
QY 2176 TTCACAAATCATACAAAAATCTTTAAATATAGAGCCCAAACTATGATTCAT 2232
Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

```

## RESULT 6

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US-10-782-570-10
; Sequence 10, Application US/10782570
; Publication NO. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1180
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
US-10-782-570-10

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## Alignment Scores:

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Pred. No.: 7,86e-87 Length: 1180
Score: 1158.00 Matches: 283
Percent Similarity: 54.55% Conservative: 131
Best Local Similarity: 37.29% Mismatches: 281
Query Match: 29.40% Indels: 64
DB: 4 Gaps: 25

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## US-10-782-570-1 (1-2235) x US-10-782-570-10 (1-1180)

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QY 13 AATAATAATGAATGAGATTATCGATTCA-----AAGAAATTTATCTTCTCTAAC 66
Db 6 AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
QY 67 AGAAATATTGATCATCTTAGATACCTTTACACAAATATCCAAATCAACCATTTACAAAC 126
Db 26 -----TyrThrArgTyrProIleGluAsnSerProLysGlnLeuLeuGlnSer 41
QY 127 ACBAATTTACAAGAGTGGCTCAATATGTGTCAAGGAATACACATATGGTGATAATTC 186
Db 42 ThrAsnTyrLysAspTyrLysAsnMetCysGlnGlnAsnGlnGlnTyrGlyLysPhe 61
QY 187 GAGACATTTGCTAGTGTGATACAAATGCTGCAGTTAGTCAGGTACTATTGTATCGGT 246
Db 62 GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValGly 78
QY 247 ACTCTGTTAGCGGTPATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGGT 306
Db 79 ThrValLeuThrGlyPheGlyPheThrThr-----ProLeuGlyLeu----- 92
QY 307 GCTATAATAATATCTTTTGGTACCTTAATCACTGTCTTTTGGCGCGGGAGACACAGAC 366
Db 93 ---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111
QY 367 AAAACAGATGACACAAATTTTAAATGGAGAAATTTTGTGTGATACACCGTTAACA 426
Db 112 AsnThr-----TrpSerAspPheIleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
QY 427 GAAAGCATAAACAGCTAAAGTTACAAACTTTAGAGGATTTAGACAAATATTACAAAGC 486
Db 131 SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150

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QY 487 TATAATACAGCATTAGATGATTCGAGAAATTAATAAAGACTACAGCTCCTGGATTACCA 546
Db 151 TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln 165
QY 547 CCATCATCAGCATTTACACAAAGCTCGCTTGAATCTTAAATATACGATTTGAGAATGTTCCAC 606
Db 166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
QY 607 AATGATTTTATTCGAGAAATACCT-----GGTTTCCAACCTTGAACTTTATAAACCGCTA 660
Db 186 ProGluLeuValAsnSerCysProAsnProSerAspCysAspTyrTyrAsnIleLeu 205
QY 661 TTACTACTATTATTCGCAAGCTGCTAAATTTTCAATTTAAATTTTATTAACAACAGGTGCT 720
Db 206 ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal 225
QY 721 GAATGGCTGATGAATGGAATGCAGATATACATCTTCCACAAATTGAACCTTAATGCTGGA 780
Db 226 LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro 244
QY 781 ACATCAGATGACTATTATAAATCTTTTAAAGAAATATATACCTAAATATAGTAATATTGT 840
Db 245 ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys 264
QY 841 GCAATACCTTATAGAGAGGACTAAATAAATCTTCGAAACGACCT----- 885
Db 265 ValThrTyrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
QY 886 ---AATATGAGATGAGATATATTAATGATTATCGAAGATATATGATCTATTCTGTATTA 942
Db 285 GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu 304
QY 943 GATACTATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATCAATAGGAAGA 1002
Db 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle----- 320
QY 1003 ATAGTGGCATTTAAACTGAACTTACAGAGAAATTTATACACTGAAATAAATTTTGAC 1062
Db 321 -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
QY 1063 CGTCTTACTTACCTTGAATTCACCAATCTCGCTATAATGGAATATAATTTTAAACAGT 1122
Db 338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
QY 1123 TCAGGGCTTAGATATTCTTTTATGATGAATATATTTTATATACAAAATGAAACG 1182
Db 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
QY 1183 TACGGGAATCGTTTAGTTGGTATTCGAATCGTAATAGATCTACTTATGCT----- 1233
Db 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
QY 1234 ACACAGAACTGAAATTTATATATGAGAAAGAAACAGCTCCACCCACACAAAACCTTTA 1293
Db 394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
QY 1294 ATACCATTTGAATTCCTATAAAGTTTCAATTTGTAATGATAGACAAAGTAACTCTTCTCC 1353
Db 414 -----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn 431
QY 1354 CTTTTTCTTAACATATCTTTTACATTTAATCAATTTGAATCTTTTAAATATTCACCT 1413
Db 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451
QY 1414 -----AGTAATAATTAACATATTTCAGCTGGGGGAATTTATCTAATGATAAAAAA 1464
Db 452 ArgLeuLeuLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470
QY 1465 ACAACTGATTTTCAATTTCTGTAAAAAAAGACTGTAAACCAATATTATTAATCCAAATGT 1524
Db 471 LysAsnIlePheGlyLeuProIleLeuLysArgGluAsnGlnGlyAsnProThrLeu 490

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QY 943 GATACCTATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGA 1002
Db 943 GATACCTATCGCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGA 1002
QY 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyTyrProIle----- 320
Db 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyTyrProIle----- 320
QY 1003 ATAGGTGGCATTAACACTGACTTACAGAGAAATTTATACAACTGAAATAAATTTGAC 1062
Db 1003 ATAGGTGGCATTAACACTGACTTACAGAGAAATTTATACAACTGAAATAAATTTGAC 1062
QY 321 -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
Db 321 -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
QY 1063 CGTCCTTACTTACCTGAAATTCACCAATCTCGCTATATATGATATATATATATATATAT 1122
Db 1063 CGTCCTTACTTACCTGAAATTCACCAATCTCGCTATATATGATATATATATATATATAT 1122
QY 338 GluSerProTyrLysTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
Db 338 GluSerProTyrLysTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355
QY 1123 TCAGGGCTTAGATATTTTCAATTTTATGATGAACTTATATTTTATACAAAAATCAAAACG 1182
Db 1123 TCAGGGCTTAGATATTTTCAATTTTATGATGAACTTATATTTTATACAAAAATCAAAACG 1182
QY 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
Db 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
QY 1183 TAGGGGAATCGTTTGTGATGTAATGGAATCGTAATAGATCTACTTATGCT----- 1233
Db 1183 TAGGGGAATCGTTTGTGATGTAATGGAATCGTAATAGATCTACTTATGCT----- 1233
QY 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
Db 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
QY 1234 ACGACAGGAACCTGAAATTTATATATATATATATATATATATATATATATATATATATAT 1293
Db 1234 ACGACAGGAACCTGAAATTTATATATATATATATATATATATATATATATATATATATAT 1293
QY 394 IleSerGlnLysSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
Db 394 IleSerGlnLysSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413
QY 1294 ATACCAATTTGAATCTCTATATAAGTTTCAATTTGTAATCTGATAGACAAGTAACCTACTTCC 1353
Db 1294 ATACCAATTTGAATCTCTATATAAGTTTCAATTTGTAATCTGATAGACAAGTAACCTACTTCC 1353
QY 414 -----GlyLeuAlaThrAsnIleTyrPheLeuLeuAsnValIleSerLeuAspAsn 431
Db 414 -----GlyLeuAlaThrAsnIleTyrPheLeuLeuAsnValIleSerLeuAspAsn 431
QY 1354 CTTTTCCTTACATATCTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCACT 1413
Db 1354 CTTTTCCTTACATATCTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCACT 1413
QY 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451
Db 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451
QY 1414 -----AGTAATAATTAACATATTCAGCTGGGGGAATTTCTAATGATATAAAAA 1464
Db 1414 -----AGTAATAATTAACATATTCAGCTGGGGGAATTTCTAATGATATAAAAA 1464
QY 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470
Db 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470
QY 1465 ACACACTGATTTCAATTTCTCTGTAATAAAGAGCTGTAAACCAATTTATTAATCCCAATTTGT 1524
Db 1465 ACACACTGATTTCAATTTCTCTGTAATAAAGAGCTGTAAACCAATTTATTAATCCCAATTTGT 1524
QY 471 LysAsnIlePheGlyLeuProIleLeuLysArgArgGluAsnGlnGlyAsnProThrLeu 490
Db 471 LysAsnIlePheGlyLeuProIleLeuLysArgArgGluAsnGlnGlyAsnProThrLeu 490
QY 1525 TPACCAAGCTAATAATAGTATATAGTATATATTTATCCAGTTTCTTTTATTTAATTTAT--- 1581
Db 1525 TPACCAAGCTAATAATAGTATATAGTATATATTTATCCAGTTTCTTTTATTTAATTTAT--- 1581
QY 491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510
Db 491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510
QY 1582 ---TCTATATAAATTTGGATTACCGCTAATATATATATATATATATATATATATATATATATAT 1638
Db 1582 ---TCTATATAAATTTGGATTACCGCTAATATATATATATATATATATATATATATATATATAT 1638
QY 511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TrpThr 523
Db 511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TrpThr 523
QY 1639 CACAGTAGTGTAAATAGAAATAATGCAATATCAGATATAAATAATTTACAAATGATCCCGCA 1698
Db 1639 CACAGTAGTGTAAATAGAAATAATGCAATATCAGATATAAATAATTTACAAATGATCCCGCA 1698
QY 524 HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrGlnIleProAla 543
Db 524 HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrGlnIleProAla 543
QY 1699 ATCAAAGGTAACAGCTTTGATACAACTCTAAGGTAATTTGAAGGACCTGGTTCATACAGGA 1758
Db 1699 ATCAAAGGTAACAGCTTTGATACAACTCTAAGGTAATTTGAAGGACCTGGTTCATACAGGA 1758
QY 544 ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563
Db 544 ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563
QY 1759 GGAACCTGGTTTATTTACAAAGTCACAGGGCTTTAGAGATTACATGATAGAACCTCTTAAT 1818
Db 1759 GGAACCTGGTTTATTTACAAAGTCACAGGGCTTTAGAGATTACATGATAGAACCTCTTAAT 1818
QY 564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
Db 564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581
QY 1819 TCTACACAACTTATTTACATAGCTTCGATACGCTACAAATGCTGCTGGAAATCTCTT 1878
Db 1819 TCTACACAACTTATTTACATAGCTTCGATACGCTACAAATGCTGCTGGAAATCTCTT 1878
QY 582 PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601
Db 582 PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601
QY 1879 CCTAATATATCTTTACAAATCCAGGAGTAATAGGAATACCACTCAACGACTCAACAAAC 1938
Db 1879 CCTAATATATCTTTACAAATCCAGGAGTAATAGGAATACCACTCAACGACTCAACAAAC 1938
QY 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620
QY 1939 ACTTTTCTGGTACAAATTAATTAATTTACAACTCGGAGATTTTGGGTATTTCCAAATTT 1998
Db 1939 ACTTTTCTGGTACAAATTAATTAATTTACAACTCGGAGATTTTGGGTATTTCCAAATTT 1998
QY 621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640
Db 621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640
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QY 1999 CCAAGTACAGTACATACCTTTAAATCGAAACATACCATTTATATATTAATCGTCGACAT 2058
Db 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
QY 2059 GTA---TCAAAATTCAAATTTTAATCAATTTGAATTTGAATTTTATACCAATTTACTTCTCT 2115
Db 661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
QY 2116 GTAGCCCAATATAGAGAAACAAAAATTTAGAACTATCCAAACAAACAAATAATATACATTT 2175
Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleIleAsnThrPhe 700
QY 2176 TTCACAAATCATACAAAAATACTTTAAATATATAGAGCCACAACTATGATATTGAT 2232
Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

RESULT 8
US-10-781-979-14
; Sequence 14, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-14

Alignment Scores:
Pred. No.: 7,86e-87 Length: 1180
Score: 1158.00 Matches: 283
Percent Similarity: 54.55% Conservative: 131
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Query Match: 29.40% Indels: 64
DB: 5 Gaps: 25

US-10-782-570-1 (1-2235) x US-10-781-979-14 (1-1180)
QY 13 AATAATAATGAATATGAGATTATCGATTCA-----AAGAAATTTATCTTCTTCTTAAC 66
Db 6 AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
QY 67 AGAATATTGATCATCTCTAGATACCTTACACAAATAATCAAAATCAACATTACAAAC 126
Db 26 -----TyrThrArgTyrProIleGluAsnSerProLysGlnLeuLeuGlnSer 41
QY 127 ACAAAATTCACAAAGAGTGCATATATGTCTCAAGGGAATACACAAATATGATATTTTC 186
Db 42 ThrAsnTyrLysAspTrpLeuAsnMetCysGlnGlnAsnGlnGlnTyrGlyGlyAspPhe 61
QY 187 GAGACATTTGCTAGTCTGATACAAATTCGTCAGGTTAGTCAGGTTACTATTGTATCCGGT 246
Db 62 GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValValGly 78
QY 247 ACTCTGTTAGCCGGTATAGTGGGCTCATCTTCTATATCCGGACCGATAGGAATAATAGGT 306
Db 79 ThrValLeuThrGlyPheGlyPheThrThr-----ProLeuGlyLeu----- 92
QY 307 GCTATATAATATCTTTTGTGTAACCTTAATCACTGTCTTTTGGCCCGGGAGAACAGAC 366
Db 307 GCTATATAATATCTTTTGTGTAACCTTAATCACTGTCTTTTGGCCCGGGAGAACAGAC 366
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Db 93 ---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111  
Qy 367 AAACAGATATGACACAAATTTATTAATGGAGAAATTTTGTGTATACACCGTTAACA 426  
Db 112 AenThr---TrpSerAspPheIleThrGlnThrLysAsnIleIleLysGluIleAla 130  
Qy 427 GAAAGCATAAACAAGCTAAAGTTACAACTTTAGAGGATTTAGACAAATATTTACAAAGC 486  
Db 131 SerThrTyrlleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150  
Qy 487 TATAATACAGCATTAGATGATGGAGAAAATTTAAAGACTACAGCTCCCTGGATTACCA 546  
Db 151 TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln 165  
Qy 547 CCATCATCAGCATYACACAGCTCCCTTGACTCTTTAAATACGATTTGAGAGTTCAC 606  
Db 166 AenThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185  
Qy 607 AATGATTTTATTCGAGAAATACCT-----GTTTCCCACTTGAACCTTATAAAGCGTA 660  
Db 186 ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu 205  
Qy 661 TTACTACTATTATATGCGAGCTGCTAATTTTCATTTTAATTTATTAACAAGGTGCT 720  
Db 206 ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisLeuThrValLeuAsnGlnAlaVal 225  
Qy 721 GAAATGGCTGATGGAATGCAGATACATATACCTTCCAAATTTGAACCTTAATGCTGA 780  
Db 226 LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro 244  
Qy 781 ACATCAGATGACTATTATAAATCTTTAAAGAAAATATACCTTAATATAGTAATCTTGT 840  
Db 245 ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys 264  
Qy 841 GCAATATCTATPAGAGAGGACTAAATAAATCTTGAACGAACT----- 885  
Db 265 ValThrTyrTyrLysGlyLeuAsnLeuIleLysThrProAspSerAsnLeuAsp 284  
Qy 886 ---AATATGAGATGGATATATTTAATGATTCGAAGATATATACCTATCTATCTATTA 942  
Db 285 GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrThrAlaValLeu 304  
Qy 943 GATACCTATCGCTCAATTTCTTTTATGATATATAAGAGATACAAAGATTCATAGAGA 1002  
Db 305 AspLeuValAlaLeuPheProAsnTyrAspValGlyLysTyrProIle----- 320  
Qy 1003 ATAGTGGCATTAACACTGAACCTTACAGAGAAATTTATPACAACTGAATAATTTGAC 1062  
Db 321 ----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337  
Qy 1063 CGTCTTACTTACCTGMAATTCACCAATCTCGCTATTAATGGAATATATTAATTAACGCT 1122  
Db 338 GluSerProTyrLysTyrTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg 355  
Qy 1123 TCAGGCTTAGATATTTTTCATTTTATGTAACCTTATATTTATACAAATAATGAACG 1182  
Db 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374  
Qy 1183 TAGGGAATCGTTAGTGTATGCGAATCGTAATGATATGATCTTATCTCT----- 1233  
Db 375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393  
Qy 1234 ACAGAGGAAGCTGAATATATATATGAGAGAAAGACAGGTCCACCCACAAACAACTTTA 1293  
Db 394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu 413  
Qy 1294 ATACCAATTTGAATCTTAAAGTTTCAATTTGTAACCTGATAGACAACTACTCTACTCT 1353  
Db 414 -----GlyLeuAlaThrAsnIleTyrIlePheLeuLeuAsnValIleSerLeuAspAsn 431  
Qy 1354 CCTTTTCTAACATATCTTACAAATTAATCAATTTGAATTTTAAATTAATTCACCT 1413  
Db 432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451

Qy 1414 -----AGTATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAA 1464  
Db 452 ArgLeuLeuGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470  
Qy 1465 ACAACTGATTTCAATTTCTGTAAAAAAGACGTGTAACCAATTTATTAATCCAAATGT 1524  
Db 471 LysAsnIlePheGlyLeuProIleLeuLysArgArgGluAsnGlnGlyAsnProThrLeu 490  
Qy 1525 TTACCAAGCTATATAGTATAGTCATATTTATCCAGTTTCTTTTATTAATATAT--- 1581  
Db 491 PheProThrTyrAspAsnTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510  
Qy 1582 ---TCCTATAAATTTGGAATTAGCGCTAAATATATATATATATACAGTGCATAGGACGA 1638  
Db 511 AlaThrTyrLys-----ThrGlnValTyrThrPheAla-----TyrThr 523  
Qy 1639 CACAGTAGTGTATAGAAATATGCAATATACAGATAAATAATATACAAATGATCCAGCA 1698  
Db 524 HisSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla 543  
Qy 1699 ATCAAGGTACACTCTTGATACAACTCTAAGGTAAATTAAGGACCTGGTCATACAGGA 1758  
Db 544 ValLysAlaAsnSerLeuGlyThrAlaSerLysValValGlnGlyProGlyHisThrGly 563  
Qy 1759 GGAACCTTGGTTTATTTTACAAAGTCAAGGGCGTTTACAGAGATTACATGTAGAACTCT 1818  
Db 564 GlyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581  
Qy 1819 TCTACAACTTATACATTTAGACTTCGATACCTGATACCTACAAATGGTGGGAATCTCT 1878  
Db 582 PheGlnGlnSerTyrPheIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601  
Qy 1879 CCTAATATCTCTTACAAATACAGGACTAATAGGAATACCACTCAACGACTCAACAAC 1938  
Db 602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro 620  
Qy 1939 ACTTTTCTGTCACAAATTAATAATTAACAATACGAGATTTTGGGTATTTCCAAATTT 1998  
Db 621 ThrPheSerGlyThrAspTyrThrAsnLeuLysTyrLysAspPheGlnTyrLeuGluPhe 640  
Qy 1999 CCAAGTACAGTAACATTAACCTTTTAAATCGAAACATACCATTTATATTAATTCGTCAGAT 2058  
Db 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660  
Qy 2059 GTA---TCAATTTCAATTTTATCATATAAATTTGAATTTATACCAATTTACTCTCTCT 2115  
Db 661 ValTyrThrAsnThrThrValIleuIleAspLysIleGluPheLeuProIleThrArgSer 680  
Qy 2116 GTACGCCCAAAATAGAGAAAAACAAAAATAGAAACTATCCAAACAAAAAATAATATCATTT 2175  
Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAsnThrPhe 700  
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Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

## RESULT 9

US-09-756-526A-4  
; Sequence 4, Application US/09756526A  
; Patent No. US20020038005A1  
; GENERAL INFORMATION:  
; APPLICANT: Jana. Wojciechowska  
; APPLICANT: Evgeny, Lewitin  
; APPLICANT: Ludmila, Revina  
; APPLICANT: Igor, Zalunin  
; APPLICANT: Galina, Cheskukhina  
; TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR.  
; FILE REFERENCE: S-30913A  
; CURRENT APPLICATION NUMBER: US/09/756,526A  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: US 60/175,158  
; PRIOR FILING DATE: 2000-01-07

; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1109  
 ; TYPE: PRF  
 ; ORGANISM: Bacillus thuringiensis  
 ; US-09-756-526A-4

Alignment Scores:  
 Pred. No.: 1.4e-65 Length: 1109  
 Score: 901.00 Matches: 240  
 Percent Similarity: 49.29% Conservative: 106  
 Best Local Similarity: 34.19% Mismatches: 242  
 Query Match: 22.87% Indels: 114  
 Ds: 3 Gaps: 27

US-10-782-570-1 (1-2235) x US-09-756-526A-4 (1-1109)

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Db	28	SerSerAspThrValAlaValSerAlaGlyIleValValGlyThrIleLeuThr	47
Qy	259	GGTATAGTGGGCTCAGTCTTATATCCGACCGATAGGAATAATAGGTGCTATATAATA	318
Db	48	-----AlaPheAlaSerPheValAsnPro-----GlyValValLeuIle	60
Qy	319	TCTTTTGTGACCTTAATCAGTCTTTTGGCCCGGGAGAACAGAC---AAACAGTA	375
Db	61	SerPheGlyThrLeuAlaProValLeuTrpProAspProGluGluAspProLysLysIle	80
Qy	376	TGGACACAAATTTATAAATGGGAATTTTGTGTATACACCGTTAAACAGAAAGCAT	435
Db	81	TrpSerGlnPheMetGlyHieGlyLeuAspLeuLeuAsnGlnThrIleSerThrAlaVal	100
Qy	436	AAACAGCTAAAGTTTACAACTTTAGACGATTTAGACAAATATTACAAAGCTATAATACA	495
Db	101	LysGluIleAlaLeuAlaHieLeuAsnGlyPheLysAspValLeuThrTyTrpGluArg	120
Qy	496	GCATTAGATGTGAGAAATTTAAAGACTACACAGCTCTCGGANTACCAACCATATCA	555
Db	121	AlaPheAsnAspTrpLysArg-----AsnProSerAla	131
Qy	556	GCATTACAAACAGCTGCTTGAATTAATACGATTTGAGATGTTTCACAAATGATTTT	615
Db	132	-----AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHiePheAsnPhe	148
Qy	616	ATTCGAGAAATACCTGGTTCCAACTTATAAAGCTTATAAAGCTTACTACTATTAT	675
Db	149	ValSerAsnMetProGlnLeuGlnLeuProThrTyTrpAspThrLeuLeuLeuSerCysTyr	168
Qy	676	CGCAGCTGCTAATTTTCAATTTAATTTATACAAAGTGTGCTGAAATGGCTGATGAA	735
Db	169	ThrGluAlaAlaAsnLeuHieLeuAsnLeuHieGlnGlyValGlnPheAlaAspGln	188
Qy	736	TGGATGCGAGATATACATCTTCAAAATTCGAATTCGATGCTGGAACATCAGATGACT	795
Db	189	TrpAsnAlaAspGlnProHieSerProMetLeuLysSerSerGlyThr-----Tyr	205
Qy	796	TATAAATTTTAAAGAAATATACCTAAATATAGTAACTATTGCAAAATACCTATAGA	855
Db	206	TyrAspGluLeuLeuValTyIleGluLysTyIleAsnTyTrpAspThrLysThrTyHis	225
Qy	856	GAAGACTATAATTAATCTCGAAACGAACCTAATATAGATGAGATGATTAATTAATGAT	915
Db	226	LysGlyLeuAsnHieLeuLysGluSerGluLysIleThrTrpAspAlaTyAsnThrTyr	245
Qy	916	CGAAGATATATGACTTACTGTATATAGTACTATCGTCAATTTCTTTTATATATATA	975
Db	246	ArgArgGluMetThrLeuIleValLeuAspLeuAlaThrPheProPheTyAspIle	265
Qy	976	AAGAGATACAAAGATTTCAATAGGAAGATAGTGGCATTAAACCTGAACTTACAGAGAA	1035
Db	266	ArgArgPhePro-----ArgGlyValGluLeuGluLeuThrArgGlu	279

Qy	1036	ATTTATACAACTGAAATAAATTTTGACCGCTTACTTACTTGAATTTCAACCAATCTC	1095
Db	280	ValTyTrpSer-----LeuAspHieLeuThrArgProGly---	292
Qy	1096	GCATATAATGGAATATAATTTAACACAGTTTCAGGGCTTAGATATTATTTTATAGTAA	1155
Db	293	-----LeuPheThrTrpLeuSerAsp	299
Qy	1156	CTTATATTTTATACAAAAATGAAACGTACGGGAATCGTTAGTTGGTATTGCGAATCGT	1215
Db	300	IleGluLeuTyThrGluSerValAlaGluGlyAspTyTrpLeuSerGlyIle-----	316
Qy	1216	AATAGATCTACTTATGCTACGACAGGAACCTGAATTT-----ATATATGGA	1260
Db	317	---ArgGluSerLysTyTrpTyTrpGlyAsnGlnPhePheThrMetLysAsnIleTyGly	335
Qy	1261	GAAAGACAGGTCCACCCACACAAAAA-----ACTTTAATACCAATTT	1302
Db	336	Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly	350
Qy	1303	GAATCTCTATAAAGTTTCAATTTGTAACCTGATAGACAACTCTACTTCCCTTTTCTCT	1362
Db	351	Glu---PheMetThrHieLeuSerIleAsnArgProPheGlnThrIleAlaGlyLeuAsn	369
Qy	1363	AACATATCTTTCAATTAATCAAAATGAACTTTTAAATAATTAATCACTAGTAATAAA	1422
Db	370	LysLeuTySerLeuIleGlnLysIle-----ValPheThrThrPheLysAsnAsp	386
Qy	1423	TTAACATATTCAGCTGGGGGAATTTATCTAATGAT-----AAAAAACCACTGAT	1473
Db	387	AsnGluTyGlnLysAsnPheAsnValAsnAsnGlnAsnGluProGlnGluThrAsn	406
Qy	1474	TTTCAATTTCTCTGTAATAAAGACTGTAAACCAATTTAATTAATCCAAATTTGTTACCAAGC	1533
Db	407	Tyr-----ProAsnAspTyTrpGlyGly	413
Qy	1534	TATATAATAGT-----TATAGTCATATTTTATCCAGATTTTCTTTTATTAATTTCTCTAT	1587
Db	414	SerAsnSerGlnLysPheLysHieAsnLeuSerHiePheProLeuIleHieLysLeu	433
Qy	1588	AAAATGGAATGAGCTGCTTAAATATATATATACAGGTGCATTTAGTACGACACAGTAGT	1647
Db	434	GluPheAlaGluTyPheHieSerIlePhe-----AlaLeuGlyTyTrpThrHieAsnSer	451
Qy	1648	GTTAATAGAAATTAATGCAATATCAGATAAATAATTAACAATGATCCACGCAATCAAAAGT	1707
Db	452	ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla	471
Qy	1708	AACAGTCTTGATCAAACTCTAAGTAAATTTGAAGGACCTCGTCAATACAGAGGAACTTG	1767
Db	472	TyrGluVal---ThrAsnAsnSerValIleArgGlyProGlyPheThrGlyGlyAspLeu	490
Qy	1768	GTTTATTTACAAAGTCAAGGGCTTTAGAGATTACATGATAGAACTCTCTAATCTTACACAA	1827
Db	491	IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys	507
Qy	1828	TCTTATTTACATTTAGACTTCTGATACGCTTACAAATTTGGTGTGGAAATACTCTTCTTAATA	1887
Db	508	LysTyTrpAlaIleSerLeuPheTyAlaAlaAsnAsnAlaIleAlaValSerIleAspVal	527
Qy	1888	TCTCTTCAATACAGAGGTAATAGGAATACCCTCAACGACTCAACACACTTTTCT	1947
Db	528	GlyAspSerGlyAlaGlyValLeu-----LeuGlnProThrPheSer	541
Qy	1948	GGTACAAATTTAATAAT-----TTACAATACGAGATTTTGGTATTTC	1992
Db	542	ArgLysGlyAsnAsnAsnPheThrIleGlnAspLeuAsnTyTrpLysAspPheGlnTyHis	561
Qy	1993	CAATTTTCCAAAGTACAGTAACATTTACCTTTTAAATCGAAACATACCATTTATATTTAATCGT	2052
Db	562	ThrLeuLeuValAspIleGluLeuProGluSerGluGluIleHieLysLeuLysArg	581







[illegible]

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QY 1156 CTTATATTTTATACAAAAAATGAAACGTCACGGAAATCGTTAGTTGGTATTCGGAATCGT 1215
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Db 300 IleGluLeuTyrThrGluSerValalaGluGlyAspTyrLeuSerGlyIle----- 316
QY 1216 AATAGATCTATCTGCTACGACGAACTGAAAT-----ATATATCGA 1260
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Db 317 ---ArgGluSerLysTyrThrGlyAsnGlnPheThrMetLysAsnIleTyrGly 335
QY 1261 GAAAGAACGGTCCACCCACACAAAA-----ACTTTAATACCAATT 1302
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Db 336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
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QY 1828 TCTTATTAATACATTAGACTTCGATACCTACAAATGGTGTGGAAATPACTCTTCTTAATATA 1887
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QY 1888 TCTCTTACAATACCGAGGATATAGGAATACCACTCAACGCTCAACACACTTTTCT 1947
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QY 1948 GGTACAATATATAAT-----TTACAATACCGAGATTTGGGTATTC 1992
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RESULT 12
US-10-782-141-17
; Sequence 17, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-17
Alignment Scores:
Pred. No.: 2,69e-65 Length: 675
Score: 897.00 Matches: 251
Percent Similarity: 47.96% Conservative: 114
Best Local Similarity: 32.98% Mismatches: 268
Query Match: 22.77% Indels: 128
DB: 4 Gaps: 32
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QY 133 TACAAGAGTCGCTCAATATGTCACAGGGAATACACAATATGGTGAATAATTCGAGACA 192
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QY 193 TTTGCTAGTCTGTATACAAATTCGTCAGTTAGTCAGGTACTATTGTATCCGTTACTCTG 252
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QY 253 TTAGCCGGTATAGTGGGCTCCTCTATATATCCGACCGATAGGAATTAATAGGTCTCTATA 312
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QY 313 ATATATCTTTTGGTACCCCTAATCACTGCTCTTTTGGCCCGGGAGAACACAGACAAACA 372
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Db 96 IleIleSerPheGlyThrLeuLeuProIlePheItrp---GlnGlySerAspProAlaAsn 114
QY 373 GTATGGACACAAATTTATTAATAATGGGAAATTTTGTGTATACACCGTTAACAGAA--- 429
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Db 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130
QY 430 -----ACGATAAAACAGCTAAAGTTACAAACTTTAGAGAGGATTTAGACAAATATACAA 483
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Db 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163
QY 544 CCACCATCATCAGCATTACACAGCTGCTTGAATCTTAAATAACGATTGAGAAATGTT 603
Db 164 -----ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrLeuGluProIle 181
QY 604 CCAAT-----GATTTATTCGAGAAATACCTCGTTTCCAACTTGAACCTTATAAA 654
Db 182 IleAspLysAspLeuAspMetLeuLysAsnAlaSerTyrArgIleProThr----- 199
QY 655 AGCTATTACTACCTATTATGCGCAAGCTGCTAATTTTCAATTAATAATTTATACACAA 714
Db 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuHis 216
QY 715 GGTGCTGAATGGCTGATGAATGCAATGCAGATATACATCTTCAAAATTTGAACCTAAT 774
Db 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233
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QY 892 AGATGGAGTATATTAATGATATTACGAAGATATATGACTATTACTGTATTAGATATATC 951
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QY 1219 AGATCTACTTATGCTACGACAGGAAGTGAATTTATATATATGAGAAAGACAGGT--- 1272
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Db 413 GluIleValArgHisArgGlu-----TyrSerAsp 422
QY 1378 ATTAATCAAAATGAACTTTTAAATAATTAATCACTAGTAAATAATTAACATATTCAGCT 1437
Db 423 IleIleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
QY 1438 GGGGGGAAATTTCTAATGATATAAAAAACAATGATTTTCAATTTCTCTGTAATAAAAAAGAC 1497
Db 442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461
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QY 1498 TGTAACCAATTATTAATCCAAATTTGTTTACCAAGCTATAATAGTATTAGTGCATATTTTA 1557
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Db 472 SerTyrIleLysThrAspAsnTyrIlePheSerVal-----ValArgGluArgArg 488
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Db 582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
QY 1969 CAATACGAGATTTGGTATTTCCTCAATTTCCAAAGTACAGTA----- 2010
Db 601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620
QY 2011 -----ACATTACCTTTAAATCGAACAATACCATTTTATATTTATTCGTGCAGATGTA 2061
Db 621 GlyGluAspThrLeuLeuMetThr-----LeuTyrGlyThrProAsnHis 635
QY 2062 TCAAAATCAATTTTAAATCATTTGATAAAATTTGAATTTTATACAAATTTCTCTCTGTACGC 2121
Db 636 SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu 654
QY 2122 CAAAATAGAGAAAAACAAAATTTAGAAACTATCCAAACAAAAATAATACATTTTTCACA 2181
Db 655 AspTyrThrGluLysGlnAsnIleGluLysThrGlnLysIleValAsnAspLeuPheVal 674
QY 2182 AAT 2184
Db 675 Asn 675

RESULT 13
US-10-782-096-18
; Sequence 18, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 675
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 12, 2006, 06:26:35 ; Search time 9 Seconds  
(without alignments)  
4695.593 Million cell updates/sec

Title: US-10-782-570-1  
Perfect score: 3939  
Sequence: 1 gtgaatcaaaataataaa.....caaaactatgatattgattaa 2235

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 134124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool.p/US10782570/runat\_12012006\_060223\_7580/app\_query.fasta\_1.2375  
-DB=Published Applications AA New -QFMT=faстан -SUFFIX=rapbn -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10782570.cgn\_1\_0 @runat\_12012006\_060223\_7580  
-NCPUS=6 -ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA New.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pap.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pap.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pap.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	716	18.2	1210	7	US-11-058-727-4
2	716	18.2	1210	7	US-11-108-389-4
3	700	17.8	652	7	US-11-192-801-4
4	699	17.7	1206	7	US-11-058-727-2
5	699	17.7	1206	7	US-11-108-389-2
6	693	17.6	652	7	US-11-192-801-6
7	691	17.5	652	7	US-11-192-801-2
8	683.5	17.4	1386	7	US-11-091-643-6
9	683	17.3	653	7	US-11-192-801-8
10	683	17.3	653	7	US-11-192-801-10

11	683	17.3	653	7	US-11-192-801-12
12	683	17.3	653	7	US-11-192-801-14
13	683	17.3	653	7	US-11-192-801-16
14	683	17.3	653	7	US-11-192-801-18
15	683	17.3	653	7	US-11-192-801-20
16	683	17.3	653	7	US-11-192-801-22
17	683	17.3	653	7	US-11-192-801-24
18	683	17.3	653	7	US-11-192-801-37
19	683	17.3	653	7	US-11-192-801-39
20	675	17.1	673	7	US-11-058-727-14
21	675	17.1	673	7	US-11-108-389-14
22	674	17.1	1316	7	US-11-091-643-4
23	665	16.9	675	7	US-11-058-727-74
24	665	16.9	675	7	US-11-058-727-80
25	665	16.9	675	7	US-11-108-389-74
26	665	16.9	675	7	US-11-108-389-80
27	664.5	16.9	674	7	US-11-058-727-82
28	664.5	16.9	674	7	US-11-108-389-82
29	664	16.9	675	7	US-11-058-727-42
30	664	16.9	675	7	US-11-058-727-48
31	664	16.9	675	7	US-11-108-389-42
32	664	16.9	675	7	US-11-108-389-48
33	663.5	16.8	674	7	US-11-058-727-50
34	663.5	16.8	674	7	US-11-108-389-50
35	662	16.8	673	7	US-11-058-727-70
36	662	16.8	673	7	US-11-108-389-70
37	661	16.8	673	7	US-11-058-727-34
38	661	16.8	673	7	US-11-058-727-68
39	661	16.8	673	7	US-11-108-389-34
40	661	16.8	673	7	US-11-108-389-68
41	660.5	16.8	674	7	US-11-058-727-76
42	660.5	16.8	674	7	US-11-108-389-76
43	660	16.8	673	7	US-11-058-727-22
44	660	16.8	673	7	US-11-058-727-64
45	660	16.8	673	7	US-11-058-727-66

ALIGNMENTS

RESULT 1  
US-11-058-727-4  
; Sequence 4, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1210  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-11-058-727-4

Alignment Scores:





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Db      607 HisAlaGlnLysThrMetAsnArgGlyGluAlaLeuThrTyrAsnLysPheAsnTyrAla 626
QY      1978 GATTTGGTATTTCCATTTCCAGTACAGTACAGTACATTTACCTTTAAATCGAAACATACCA 2037
Db      627 ThrLeuProProIleLysPheThrThrThrGlu-----Pro 638
QY      2038 TTT-----ATATTTAATCGTGCAGATGTATCAAAATTCATTTTAAATCATT 2082
Db      639 PheIleThrLeuGlyAlaIlePheGluAlaGluAspPheLeuGlyIleGluAlaTyrIle 658
QY      2083 GATAAATGATTTATACCAATTTACTTCTCTGTACGCCAAATPAGAGAAAACAAAAA 2142
Db      659 AspArgIleGluPheIleProValAspGluThrTyr-----GluAlaGluGlnAsp 675
QY      2143 TTGAAACTATCCAAACAAATAATACATTTTTCACAAATCATACAAAATACTTTA 2202
Db      676 LeuGluAlaAlaLysLysAlaValAsnAlaLeuPheThrAsn---ThrLysAspGlyLeu 694
QY      2203 AATATAGAAGCCACAAACTATGATATTGAT 2232
Db      695 ArgProGlyValThrAspTyrGluValAsn 704

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# RESULT 2

US-11-108-389-4

; Sequence 4, Application US/11108389

; Publication No. US20050261188A1

## GENERAL INFORMATION:

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; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu

```

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

; FILE REFERENCE: 35718/291049

; CURRENT APPLICATION NUMBER: US/11/108,389

; PRIOR FILING DATE: 2005-04-18

; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26

; PRIOR APPLICATION NUMBER: 60/460,787

; PRIOR FILING DATE: 2003-04-04

; PRIOR APPLICATION NUMBER: 10/606,320

; PRIOR FILING DATE: 2003-06-25

; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 1210

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-11-108-389-4

## Alignment Scores:

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Pred. No.:      8,596-48      Length:      1210
Score:           716.00      Matches:      216
Percent Similarity: 44.81%      Conservative: 138
Best Local Similarity: 27.34%      Mismatches: 304
Query Match:      18.18%      Indels:      132
DB:              7          Gaps:        30

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US-10-782-570-1 (1-2235) x US-11-108-389-4 (1-1210)

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QY      1 GTGAATCAAAATAAATAATCAATATGAGATTATCGATTCAAGAAATTTATCTTATCCT 60
Db      1 MetSerProAsnAsnGlnAsnGluTyrGluIleIleAspAlaThrProSerThrSerVal 20
QY      61 TCTAACAGAAATPATTGATCATTTCTAGATACCCCTTACACAAATAAATCCAAATCAACCATTA 120
Db      21 SerAsn-----AspSerAsnArgTyrProPheAlaAsnGluProThrAsnAlaLeu 37

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```

QY      121 CAAACACAAATTTACAAAGAGTGGCTCAATATGTGTCAAGGAAT---ACACAATATGCT 177
Db      38 GlnAsnMetAspTyrLysAspTyrLeuLysMetSerAlaGlyAsnAlaSerGluTyrPro 57
QY      178 GATAATTTCCGACATTTTGTAGTCTGATACAAATGTCTGCAGTTAGTGCAGGTACTATT 237
Db      58 GlySerProGluValLeuValSerGlyGlnAsp-----AlaAlaLysAlaAlaIleAsp 75
QY      238 GTATCCGGTACTCTGTAGCCGGTATAGTGGGTCTCACTTCTATATCCGACCGATAGGA 297
Db      76 IleValGlyLysLeuLeuSerGlyLeuGly-----ValPro 87
QY      298 ATAATAGGTGCTATAATAATATCTTTTGGTACCCTTAATCACTGTCTTTTGGCCCGCGGA 357
Db      88 PheValGlyProIleValSerLeuTyrThrGlnLeuIleAspIleLeuTyrProSerGly 107
QY      358 GAACAAGACAAAACAGTATGACACAAATTTATAAATGGGAGAAATTTTGTGTGATACA 417
Db      108 Gln-----LysSerGlnTyrGluIlePheMetGluGlnValGluGluLeuIleAsnGln 125
QY      418 CCGTTACAGAAAGCATAAACAGCTAAAGTTACAACCTTTTGAAGGATTTAGACAAATA 477
Db      126 LysIleAlaGluTyrAlaArgAsnLysAlaLeuSerGluLeuGluGlyLeuGlyAsnAsn 145
QY      478 TTACAAAGCTATAATACAGCATTTAGATGATTGGAGAAAATTTAAAAAGACTACAAAGCTCT 537
Db      146 TyrGlnLeuTyrLeuThrAlaLeuGluGluTyrLysGlu----- 158
QY      538 GGATTACCAACCATCATCAGCATTTACAAACAGCTGCTTTGACTCTTTAAATACGATTTGAG 597
Db      159 -----AsnProAsnGlySer-----ArgAlaLeuArgAspValArgAsnArgPheGlu 174
QY      598 AATGTTCAATGATTTTATTCGAGAAATATACCTGTTTCCAACTTGAACCTTATAAAGC 657
Db      175 IleLeuAspSerLeuPheThrGlnTyrMetProSerPheArgValThrAsnPheGluVal 194
QY      658 CTATTACTACCTATTATGCGCAAGCTGCTCAATTTTCAATTTTAAATTTTATTTACAAACAGT 717
Db      195 PropheLeuThrValTyrThrGlnAlaAlaAsnLeuHisLeuLeuLeuLeuLysAspAla 214
QY      718 GCTGAATTTGGTGAATGGAATGCAGATATACATCTCTTCACAAATTTGAACCTAATGCT 777
Db      215 SerIlePheGlyGluGluTyrGlyTrp-----SerThr 225
QY      778 GGAACATCAGATGACTATTATAAATTTTAAAGAAATATACCTTAAATATAGTAACTAT 837
Db      226 ThrThrIleAsnAsnTyrTyrAspArgGlnMetLysLeuThrAlaGluTyrSerAspHis 245
QY      838 TGTGCAATACCTATAGAGAGGACTAAATAAATTCGAAACGAACTTAATATGATGATGG 897
Db      246 CysValLysTyrTyrGluThrGlyLeuAlaLysLeuLysGlyThrSerAlaLysGlnTyr 265
QY      898 AGTATATTATTAATGATATATCGAAGATATATGACTATTACTGTATTAGTACTATCGCTCAA 957
Db      266 ValAspTyrAsnGlnPheArgArgGluMetThrLeuThrValLeuAspValValAlaLeu 285
QY      958 TTTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAGAAATAGGTGGCAATTAAA 1017
Db      286 PheProAsnTyrAspThrArgThrTyrProMetGlu-----ThrLys 299
QY      1018 ACTGAACCTTACAAGAGAAATTTATCAACT-----GAAATAAATTTTGCACGCTCT 1068
Db      300 AlaGlnLeuThrArgGluValTyrThrAspProLeuGlyAlaValAsnValSerSerIle 319
QY      1069 ---ACTTACCTTTGAAATTTCAACCCCAATCTCGCTATAATGGAATATAATTTTAAACGTTCA 1125
Db      320 GlySerTyrTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro 339
QY      1126 GGGCTTAGATTTATTTTCACTTTTGTAGTGAACCTTATTTATTTATACAAAATAAAGACG--- 1182
Db      340 Pro---HisValPheAspTyrIleThrGlyLeuThrValTyrThrGlnSerArgSerIle 358

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139 AsnAsnPheGluAspTyrValAsnAlaLeuAsnSerTrpLysLys----- 153  
Qy GCTCTGATTTACACCATCATCAGCATTAACAACAGCTGCTTGAATACGA 591  
Db -----ThrProLeuSerLeuArgSerLysArgSerGlnAspArgGluLeu 170  
Qy TTTGAGAAATGTTCAATGATTTATTCGAGAAATACCTGCTTCCCAATCGAAATCTAT 651  
Db -----PheSerGlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPhe 190  
Qy AAAACGCTATTACTACCTATTATGCGCAAGCTGCTAAATTTTCAATTTTAAATTTATACAA 711  
Db -----GluValLeuPheLeuProThrTyrAlaGlnAlaAlaAsnThrHisLeuLeuLeuLys 210  
Qy CAAGTGTGTAATGGCTGATGATGGAATGCAGATATACATCTTCACAAATGGAACCT 771  
Db -----AspAlaGlnValPheGlyGluTrpGlyTyrSer----- 222  
Qy AATGCTGGAACATCAGATGACTATTATAAACTTTTAAAAAGAAATATACCTAAATATAGT 831  
Db -----SerGluAspValAlaGluPheTyrHisArgGlnLeuLysLeuThr--GlnGlnTyrThr 241  
Qy AACTATTGTGCAATACCTATAGAGAAGGACTAAATAAATTCGAAACGAACCTAATATG 891  
Db -----AspHisCysValAsnTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyrAsp 261  
Qy AGATGGAGTATTATTAATGATTTCGAAGATATATGACTATTACTATTAGTATTAGATATATC 951  
Db -----AlaTrpValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeuIle 281  
Qy GCTCAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGATAGGTGGC 1011  
Db -----ValLeuPheProPheTyrAspValArgLeuTyrSerLys-----Gly 295  
Qy ATTTAACTGAATTTACAGAAATTTATACAACTGAATTAATTTTACCGTCTTACT 1071  
Db -----ValLysThrGluLeuThrArgAspPheThrAspProIle--PheSerLeuAsnThr 314  
Qy TACCTTGAATTCACCAATCTCGTATATATGGAATATATTTAAACAGTTCAGGGCTT 1131  
Db -----LeuGlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro----- 332  
Qy AGATTATTTTCAATTTTATAGTGAATCTATATTTTATACAAA----- 1173  
Db -----HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrSer 352  
Qy -----AATGAAACGTACCGGAATCGTTTGTGTTATTCGGAATCGTAAT 1218  
Db -----GlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArgPro 369  
Qy AGATCTACTATGCTACGACGAACTGMAATATATATATGGAAGAAGACAGGTCCACC 1278  
Db -----SerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGluPro 389  
Qy ACAACAAACAACTTTAATCACTTCAATCTTAAATGTTCAATGTTAATGATAGACAA 1338  
Db -----ValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----ArgThr 403  
Qy GTA-----ACTCTACTTCTCCCTTTTCTCTAC-----ATATACTTTTACAAATTAATCA 1386  
Db -----IleAlaAsnThrAspValAlaAlaTrpProAsnGlyLysIleTyrPheGlyValThrLys 423  
Qy ATTGAATTTTAAATTAATTCACCTAGTATAAATTA-----ACATATTCAGCT 1437  
Db -----ValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAspSer 443  
Qy -----GGGGGAATTTTATCTAATGATAAA-----AAAAA 1467  
Db -----LysArgAsnAsnGlyHisValGlyAlaGlnAspSerIleAspGlnLeuProGluThr 463  
Qy ACTGATTTTCAATTTCTCTGTAATAAAGACTGTAACCAATTTATTAATCAATTTGTTTA 1527  
Db -----GluProLeuGluLys----- 470

1528 CCAAGCTATAATAGTATAGTATATTTATTTATCCAGTTTCTTTATTTAATTTATTCCTAT 1587  
Db -----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAsp 486  
Qy AAAATTCGATAGCGCTAAATATATATATATATATACAGGTGCTAGGATGACACACAGTAGT 1647  
Db -----ArgArgGlyThrIle-----ProPhePheThr-----TrpThrHisArgSer 500  
Qy GTTAAATAGAAATATGCAATATCAGATAAAATATTAATTAATGATCCAGCAATCAAAAGT 1707  
Db -----ValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValLysAla 520  
Qy AACAGTCTTGATACAAATCTTAAGCTAATTAAGAGCACTGCTCATACAGGAGGAACTTG 1767  
Db -----TyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsnLeu 540  
Qy GTTTATTTTACAA-----AGTCAAGGGCGTTTATAGATTTACATGTAGAACTCCT 1815  
Db -----LeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSerAla 560  
Qy AATTCTACACATCTTATTACATTTAGACTTCGATCGATCAATGCTGCTGCTGGAATACT 1875  
Db -----AlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 575  
Qy CTTCCTAATATCTCTTACAAATACAGGAGTAAATAGGAATACCACTCAACGACTCAAC 1935  
Db -----ThrAsnLeuArgLeuPheVal-----GlnAsnSerAsn 586  
Qy AACACTTTTCTGCTACAAATTTAATTAATTTACAATAC-----GGAGATTTTGGGTAT 1989  
Db -----AsnAspPheIleValIleTyrIleAsnLysThrMetAsnIleAspAspLeuThrTyr 606  
Qy TTCCAATTTCCAGTACAGTAACTTACCTTTAATTCGAACATACCACTT----- 2040  
Db -----GlnThrPheAspLeuAlaThrThr-----AsnSerAsnMetGlyPheSerGlyAsp 623  
Qy -----ATATTTAATCGTGCAGATGTATCAAAATTCAAATTTCAATTTAATCATTCAT 2085  
Db -----ThrAsnGluLeuIleIleGlyAlaGluSerPheValSerAsnGluLysIleTyrIleAsp 643  
Qy AAAATTCGAATTTATACCAAT 2106  
Db -----LysIleGluPheIleProVal 650  
RESULT 4  
US-11-058-727-2  
; Sequence 2, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flanagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; PRIORITY FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIORITY FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIORITY FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIORITY FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2





Db 320 GlySerTrpTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro 339  
 QY 1126 GGCCTTAGATATTTTTCATTTTATGACGAACTTATATTTTATACAAAATAAGAAAGTAC 1185  
 Db 340 Pro---HisValPheAspTyrIleThrGlyLeuThrValTyrThrGlnSerArgSerIle 358  
 QY 1186 GGGAAAT---CGTTAGTTGGTATTGCGAATCCTAATAGATCTACTTAT---GCTACG 1236  
 Db 359 SerSerAlaIleArgTyrIleArgHisTrpAlaGlyHisGlnIleSerTyrHisArgValSer 378  
 QY 1237 ACAGAACTGAAATTT---ATATATGAGAAAGAACAGCTGCCACCAACAACT 1290  
 Db 379 ArgGlySerAsnLeuGlnMetTyrGlyThrAsnGlnAsnLeuHisSerThrSerThr 398  
 QY 1291 TTAATACCATTTGAATCTCTATAAGTT---TCATTTGTAACGTATAGACAAAGTAACTCCT 1347  
 Db 399 ---PheAspPheThrAsnTyrAspIleTyrLysThrLeuSerLysAspAlaValLeuLeu 417  
 QY 1348 ACTTCCCTTTTCTTAAC---ATATACTTTTACAATTAATCAAAATGAACCTTAT 1398  
 Db 418 AspIleValTyrProGlyTyrThrTyrIlePhePheGlyMetProGluValGluPhePhe 437  
 QY 1399 TTAATAAATCACCTAGTAAATAATTAACATATTCAGCTGGGGGAATTTATCTAATGAT 1458  
 Db 438 MetValAsn---GlnLeuAsnAsnThr 445  
 QY 1459 AAAAAACAACTGATTTTCAATTTCTGTAAAAAGACTGTAAACCAATTTAATCCA 1518  
 Db 446 ArgIlySerThrLeuLysTyrAsn---ProValSerLysAspIleIleAlaSerThrArgAsp 464  
 QY 1519 AATTGTTTA---CCAAGCTATAATAGTTATAGTCAT 1551  
 Db 465 SerGluLeuGluLeuProGluThrSerAspGlnProAsnTyrGluSerTyrSerHis 484  
 QY 1552 ATTTATCCCAAGTTTCTTTATTTAATTTATCTTATAAAATTTGGATTAGCGCTAAATATA 1611  
 Db 485 ArgLeuCysHisIleThr-----SerIle 492  
 QY 1612 TTATATACAGT-----GCATTAGAGTGCACACACAGTAGTGT 1650  
 Db 493 ProAlaThrGlyAsnThrThrGlyLeuValProValPheSerTrpThrHisArgSerAla 512  
 QY 1651 AATAGAATAATGCAATATCAGATAAATAATTAACAATATCCAGCAATCAAAAGGTAAC 1710  
 Db 513 AspLeuAsnAsnThrIleTyrSerAspLysIleThrGlnIleProAlaValIleCysTrp 532  
 QY 1711 AGCTTTGATCAAACTCTAAGGTAATGAAGACCTGGTTCATACAGGAGGAACTGGTT 1770  
 Db 533 AspAsnLeuProPheValProValValLysGlyProGlyHisThrGlyGlyAspLeuLeu 552  
 QY 1771 ---TATTTACAACTCAAGG-----CGT 1791  
 Db 553 GlnTyrAsnArgSerThrGlySerValGlyThrLeuPheLeuAlaIleArgTyrGlyLeuAla 572  
 QY 1792 TTAGAGATTACATGTAGAAGTCTTAATCTTACAACTCTTATTATTAATAGATTTCGATAC 1851  
 Db 573 LeuGlu-----LysAlaGlyLysTyrArgValArgValGluArgTyr 585  
 QY 1852 GCTCAAAATGGTGTGGAAATPACTCTTCTTAATATCTCTTACAATACCCAGGAGTAATA 1911  
 Db 586 AlaThrAspAla-----AspIleValLeuHisValAsnAspAlaGln 599  
 QY 1912 GGAATACCACTCAACGACTCAACACACACTTTTCTGTGTACAAATTAATAATTTACAA 1971  
 Db 600 IleGlnMetProLysThrMetAsnProGly-----GluAspLeuThr 613  
 QY 1972 TACGAGATTTTGGTATTCTCCATTTTCCAAAGTACAGTAACATTACCTTTTAAATCGAAAC 2031  
 Db 614 SerLysThrPheLysValAlaAspAlaIleThrThrLeuAsnLeuAlaThrAspSerSer 633  
 QY 2032 ATACCAATTTATTTAATCGGACAGATGTATCAAAATTTCA-----ATTTAATC 2079  
 Db 634 LeuAlaLeuLysHisAsnLeuGlyGluAspProAsnSerThrLeuSerGlyIleValTyr 653

QY 2080 ATTGATAAAATTTGAATTTATACCAATTAATCTCTCTGTACGCCAAAATAGAGAAAACAA 2139  
 Db 654 ValAspArgIleGluPheIleProValAspGluThrTyr-----GluAlaGluGln 670  
 QY 2140 AAATTAGAAACTATCCAAACAAATAAATACATATTTTTCACAAATCATACAAAAAATACT 2199  
 Db 671 AspLeuGluAlaIleLysLysAlaValAsnAlaLeuPheThrAsn---ThrLysAspGly 689  
 QY 2200 TTAATAATAGAACCCAAACTATGATATTGAT 2232  
 Db 690 LeuArgProGlyValThrAspTyrGluValAsn 700  
 RESULT 6  
 US-11-192-801-6  
 ; Sequence 6, Application US/11192801  
 ; Publication No. US20050273882A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Romano, Charles P.  
 ; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
 ; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
 ; CURRENT APPLICATION NUMBER: US/11/192,801  
 ; CURRENT FILING DATE: 2005-07-29  
 ; PRIOR APPLICATION NUMBER: US/10/232,665  
 ; PRIOR FILING DATE: 2002-08-29  
 ; PRIOR APPLICATION NUMBER: US/09/377,466  
 ; PRIOR FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 652  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic or  
 ; FEATURE: non-naturally occurring amino acid sequence encoded by SEQ ID NO:  
 ; NAME/KEY: PRT  
 ; LOCATION: (1)..(652)  
 ; US-11-192-801-6  
 Alignment Scores:  
 Pred. No.: 4-5e-46 Length: 652  
 Score: 693.00 Matches: 208  
 Percent Similarity: 44.84% Conservative: 122  
 Best Local Similarity: 28.26% Mismatches: 286  
 Query Match: 17.59% Indels: 120  
 DB: 7 Gaps: 28  
 US-10-782-570-1 (1-2235) x US-11-192-801-6 (1-652)  
 QY 1 GTCGAATCAAAATAATTAATGAATATGAGATTATCGATTCAAGAATTTATCTTATCCT 60  
 Db 1 MetAsnProAsnAsnArgSerGluHisAspThrIle-----LysValThrProAsn 17  
 QY 61 TCTAAACAGAAATATTGATCATCTTACATACCTTACCAATAATCAATAATCAACCATTA 120  
 Db 18 SerGluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeu 37  
 QY 121 CAAACACACAAATATCAAAAGAGTGGCTCAATATGTGTCAA---GGGAATACACAATATGGT 177  
 Db 38 GluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeu 57  
 QY 178 GATAAATTCGAGACATTTTGTCTAGTGTGATACAATTTGCT---GCAGTTAGTCAGGTPACT 234  
 Db 58 AspAsn-----SerThrValLysAspAlaValGlyThrGlyIle 70  
 QY 235 ATTGTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATA 294  
 Db 71 SerValValGlyGlnIleLeuGlyValValGly-----Val 82  
 QY 295 GGAATAATAGGTCTCTATAATAATATCTTTTGGTACCCCTAATCACTGTCTTTTGGCCGCG 354

Db 83 PropheAlaGlyAlaLeuThrSerPheTyGlnSerPheLeuAenThrIleTrpProSer 102  
QY 355 GGAGAACAGACAAACAGTAGTGGACACAAATTTATTAATAATGGGAGAAATTTTGTTCAT 414  
Db 103 -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAsp 119  
QY 415 ACACGGTTAACAGAACGATATAACAGCTAAAGTTTACAACTTTTGAAGAGGATTTAGACAA 474  
Db 120 LysLysIleGluGluTyAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAen 139  
QY 475 ATATTACAAAGCTATAATACAGCATTAGATGATGAGAAATTTAAAGAGCTACAGCT 534  
Db 140 AenPheGluAspTyValAenAlaLeuAenSerTrpLysLys----- 153  
QY 535 CTGGATTACACACCATCATCAGCATTACAAACAGCTGCTTGAATCTTAAATACGATTT 594  
Db 154 -----ThrProLysSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPhe 171  
QY 595 GAGATGTTCAATGATTTTATTTCGAGAAATACCTGCTTTCCAACTTGAACCTTATATAA 654  
Db 172 SerGlnAlaGluSerHisPheArgAenSerMetProSerPheAlaValSerLysPheGlu 191  
QY 655 AGCTATTATACCTATTATGCGCAAGCTGCTAATTTTCAATTTTAAATTTTATACAA 714  
Db 192 ValLeuPheLeuProThrTyAlaGlnAlaAenThrHisLeuLeuLeuLysAsp 211  
QY 715 GGTGCTGAATGGCTGATGAATGGAATGCAGATATACATCTTCACAAATTCGAACCTAAT 774  
Db 212 AlaGlnValPheGlyGluGluTrpGlyTySer-----Ser 223  
QY 775 GCTGGAACATCAGATGACTATTATAAATCTTTAAAGAAATATATACCTTAATATAGTAAC 834  
Db 224 GluAspValAlaGluPheTyHisArgGlnLeuLysLeuThr--GlnGlnTyThrAsp 242  
QY 835 TATTGTCANAATACCTATAGAGAGGACTAATAAATCTTGAACGAACTTAAATATAGAGA 894  
Db 243 HisCysValAenTrpTyAsnValGlyLeuAenGlyLeuArgGlySerThrTyAspAla 262  
QY 895 TGGAGTATATTATGATTATCGAGATATATGACTATTATGCTATATAGATACATCGCT 954  
Db 263 TrpValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeuIleVal 282  
QY 955 CAATTTCTTTTATGATATAAGAGATACAAAGATTCATAGGAAGATAGGTGGCAT 1014  
Db 283 LeuPheProPheTyAspIleArgLeuTySerLys-----GlyVal 296  
QY 1015 AAACTGAATACAGAGAAATTTATCAACTGAAATATAATTTTGCCTTCTTACTTAC 1074  
Db 297 LysThrGluLeuThrArgAspIlePheThrAspProIle---PheSerLeuAenThrLeu 315  
QY 1075 CTTGAAATTCACCCCAATCTCGCTATATATGATATATTAACACGTTTCAGGGCTTAGA 1134  
Db 316 GlnGluTyGlyProThrPheLeuSerIleGluAenSerIleArgLysPro-----His 333  
QY 1135 TTATTTTCATTTTATAGTGAATATTTTATATACAAA----- 1173  
Db 334 LeuPheAspTyLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyPheGly 353  
QY 1174 -----AATGAAACGTACCGGAATCGTTTGTAGTTTGGTATTCGAATCGTAATAGA 1221  
Db 354 LysAspSerPheAenTyTrpSerGlyAenTy-----ValGluThrArgProSer 370  
QY 1222 TCTACTTATGCTACAGAGAACTGAAATATATATGAGAGAAAGACAGGTCCACCCACA 1281  
Db 371 IleGlySerSerLysThrIleThrSerProPheTyGlyAspLysSerThrGluProVal 390  
QY 1282 ACACAAACTTTAATACCTTCAATCCATATATGATTTCAATGTAAGTACGATAGACAGTA 1341  
Db 391 GlnLys-----LeuSerPheAspGlyGlnLysValTy-----ArgThrIle 404  
QY 1342 -----ACTCCTACTTCCCTCTTTCTTCAAC-----ATATACTTTTCAATTAATCAAT 1389  
Db 405 AlaAenThrAspValAlaAlaTrpProAenGlyLysValTyLeuGlyValThrLysVal 424

QY 1390 GAACCTTTTAAATAATTCACCTAGTAGTAATAATTA-----ACATATTTCAGCT--- 1437  
Db 425 AspPheSerGlnTyAspAspGlnLysAenGluThrSerThrGlnThrTyAspSerLys 444  
QY 1438 -----GGGGGGAATTTATCTAATGTATATAAAAAACAACCTGATTTTCAATTTCTCTGTA 1491  
Db 445 ArgAenAenGlyHisValSerAlaGlnAspSerIleAsp-----GlnLeuProGlu 462  
QY 1492 AAAGACTGTAAACCAATTTAATCCAAATTTGTTTACCAGCTATATATAGTATAGTCAAT 1551  
Db 463 ThrThrAspGluProLeu-----GluLysAlaLysSerHis 474  
QY 1552 ATTTTATCCCAAGTTTCTTTTATTTAAATTTATCTTATAAATTCGATTAGCGCTAAATATA 1611  
Db 475 GlnLeuAenTyAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle-----Pro 492  
QY 1612 TTATATACAGCTGATAGGATGACACACAGTAGTGTATATAGAAAATAATGCAATATCA 1671  
Db 493 PhePheThr-----TipThrHisArgSerValAspPhePheAenThrIleAsp 508  
QY 1672 GATATAAATAATTAATGATCCAGCAATCAAGGTAAACAGCTCTTGATACAACTCTAAG 1731  
Db 509 AlaGluLysIleThrGlnLeuProValLysAlaTyAlaLeuSerSerGlyAlaSer 528  
QY 1732 GTAATTGAAGACCTGGTCATACAGAGGAACTTGGTTTATTTTACAA----- 1779  
Db 529 IleIleGluGlyProGlyPheThrGlyAenLeuLeuPheLeuLysGluSerSerAen 548  
QY 1780 AGTCAAGCGCGTTAGAGATTACATGTAGAACTCTTAATCTTACACAACTTATTACATT 1839  
Db 549 SerIleAlaLysPheLysValThrLeuAenSerAlaAlaLeuLeuGlnArgTyArgVal 568  
QY 1840 AGACTTCGATACGCTACAAATGGTCTGGAATACTCTCTTAATATATCTCTTACAATA 1899  
Db 569 ArgIleArgTyAlaSerThr-----ThrAenLeuArgLeuPheVal 582  
QY 1900 CCAGGAGTAATAGGAATACCACCTCAACGACTCAACACACTTTTCTGTTACAAATAT 1959  
Db 583 -----GlnAenSerAenAenAspPheLeuValIleTyIle 594  
QY 1960 AAT-----AATTTACAAATACGAGATTTTGGGTATTTTCCAATTT 1998  
Db 595 AsnLysThrMetAenLysAspAspLeuThrTyAsnThrPheAspLeuAlaThrThr 614  
QY 1999 CCAAGTACAGTAACTTACCTTTAAATCGAAACATACCATTTATTTAATTCGTGCAGAT 2058  
Db 615 AenSerAenMetGlyPheSerGlyAspLysAenGluLeuIleIleGlyAlaGluSerPhe 634  
QY 2059 GTATCAAAATTTCAATTTAATCAATGATAAAATTTGAATTTATATATCAAT 2106  
Db 635 ValSerAenGluLysIleTyIleAspLysIleGluPheIleProVal 650

## RESULT 7

US-11-192-801-2  
; Sequence 2. Application US/11192801  
; Publication No. US20050273882A1  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 652  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis



















Qy	949	ATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGATAGGT	1008
Db	282	IlleValLeuPheProPheTyArgPilleArgLeuTySerLys	295
Qy	1009	GGCATTAATAACTGAACCTTACAAGAGAAATTTATACAACCTGAATAAATTTTGACGCTCTT	1068
Db	296	GlyValIleThrGluLeuThrArgAspIlePheThrAspProIlePheLeuLeuThr	314
Qy	1069	ACTTACCTTGAAATTCACACCAATCTCGCTATATATGAATATATATTAACACGCTTCAGGG	1128
Db	315	ThrLeuGlnLysTyGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro	333
Qy	1129	CTTAGATTATTTTCATTTTATAGAACTTATATTTATATATATTTATACAAA	1173
Db	334	HisLeuPheAspTyLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTy	352
Qy	1174	ANTGAACGTCAGCGGAATCGTTAGTTGGTATTCGGAATCGT	1215
Db	353	PheGlyLysAspSerPheAsnTyTrpSerGlyAsnTy	369
Qy	1216	AATAGATCTACTTATGCTACGACGAGAACTGAAATTTATATATATGAGAGAAAGAACAGCTCCA	1275
Db	370	ProSerIleGlySerSerLysThrIleThrSerProPheTyGlyAspLysSerThrGlu	389
Qy	1276	CCACAAACAAAACCTTTTAATACCATTTGAATCTCTATAAAGTTTCAATGTGTAACCTGATAGA	1335
Db	390	ProValGlnLysLeuSerPheAspGlyGlnLysValTy	403
Qy	1336	CAAGTAACTCCTACTTCCCCTTTTCTCAACATATACITTTTCAATTAAT	1383
Db	404	ThrIleAlaAsnThrAspValAlaIleThrProAsnGlyValTyLeuGlyValThr	423
Qy	1384	CAAAATGAACTTTATTTAAATAAATTCACCTAGTAATAAATA	1434
Db	424	LysValAspPheSerGlnTyAspAspGlnLysAsnGluThrSerThrGlnThrTyArg	443
Qy	1435	GCTGGGGGAATTTATCTAATGATAAAAAACAACACTGATTTTCAATTCCT	1485
Db	444	SerLysArgAsnAsnGlyHisValSerAlaGlnAspSerIleAsp	461
Qy	1486	GTAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTCACAGCTATAATAGTTAT	1545
Db	462	ProGluThrThrAspGluProLeu	473
Qy	1546	AGTCATATTTATCCCAAGTTTCTTTTATTTAATTTATTCCTATAAAATGGATTAGCGCTA	1605
Db	474	SerHisGlnLeuAsnTyAlaGluCysPheLeuMetGlnAspArgGlyThrIle	492
Qy	1606	AATATATATATACAGGTGCATTTAGGATGACACACAGTAGTGTGTAATAGAAATATGCA	1665
Db	493	ProPhePheThrTrpThrHisArgSerValAspPhePheAsnThr	507
Qy	1666	ATATCAGATAAATAATTTACAATGATCCACAGCAATCAAAGTAAACAGCTTTGATACAAAC	1725
Db	508	IleAspAlaGluLysIleThrGlnLeuProValValLysAlaTyAlaLeuSerSerGly	527
Qy	1726	TCTAAGGTAAATGAAGACCTGGTCATACAGGAGAAACTTGGTTTATTACAA	1779
Db	528	AlaSerIleIleGluGlyProIlePheThrGlyGlyAsnLeuLeuPheLeuLysGluSer	547
Qy	1780	AGTCNAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTTCTACACATCTTAT	1833
Db	548	SerAsnSerIleAlaLysPheLysValThrLeuAsnSerAlaLeuLeuGlnArgTy	567
Qy	1834	TACATTAGACTTCGATACGCTACAAATGGTCTGGAATACTCTTCCTAATAATATCTCTT	1893
Db	568	ArgValArgIleArgTyAlaSerThr	581
Qy	1894	ACAATACAGGAGTAATAGGAATACCACTCAACGCTCAACAACTTTTCTGGTGACA	1953
Db	582	PheValGlnAsnSerAsnAspPheLeuValIle	593

Qy 1954 AATTATTAAT-----AATTACAATACGAGATTTCGGTATTTC 1992  
Db 594 TyrIleAsnLysThrMetAsnLysAspAspLeuThrTyThrGlnThrPheAspLeuAla 613  
Qy 1993 CAATTTCCAGTACAGTAACATTACCTTTAAATCGAAACATACCATTTTATATTTAATCGT 2052  
Db 614 ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuIleGlyAlaGlu 633  
Qy 2053 GCAGATGTATCAAAATTCAAATTTAAATCAATGATAAAATTTGAATTTATATCAAAAT 2106  
Db 634 SerPheValSerAsnGluLysIleTyIleAspLysIleGluPheIleProVal 651

RESULT 13  
US-11-192-801-16  
; Sequence 16, Application US/11192801  
; Publication No. US20050273882A1  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 653  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PRT  
; LOCATION: (1)..(653)  
; OTHER INFORMATION: Cry3Bb1 variant v11231  
US-11-192-801-16

Alignment Scores:  
Pred. No.: 2,63e-45 Length: 653  
Score: 683.00 Matches: 207  
Percent Similarity: 44.58% Conservative: 122  
Best Local Similarity: 28.05% Mismatches: 283  
Query Match: 17.34% Indels: 126  
DB: 7 Gaps: 28

US-10-782-570-1 (1-2235) x US-11-192-801-16 (1-653)  
Qy 4 AATCAAAATAATAATGAATATGAGATTATCGATTCAAGAAATTTATCTTATCTCTTCT 63  
Db 3 AsnProAsnAsnArgSerGluHisAspThrIle-----LysValThrProAsnSer 19  
Qy 64 AACGAAATATTGATCATTTCTAGATACCGTTACAAATAATCCAAATCAACATTACAA 123  
Db 20 GluLeuGlnThrAsnHisAsnGlnTyProLeuAlaAspAsnProAsnSerThrLeuGlu 39  
Qy 124 AACCAAAATTCACAAAGAGTGGCTCAATATGTCTCAA---GGGAATACAAATATGGTGTAT 180  
Db 40 GluLeuAsnTyLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeuAsp 59  
Qy 181 AATTTTCGAGACATTTTGTCTAGTCTGATACAAATTTGCT---GCAGTTAGTCGAGTACTATT 237  
Db 60 Asn-----SerThrValLysAspAlaValGlyThrGlyIleSer 72  
Qy 238 GTATCCGGTACTCTCTTATAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGA 297  
Db 73 ValValGlyGlnIleLeuGlyValValGly-----ValPro 84  
Qy 298 ATAATAGTGTCTATATAATATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGCGGA 357  
Db 85 PheAlaGlyAlaLeuThrSerPheTyThrGlnSerPheLeuAsnThrIleLysProSer--- 103  
Qy 358 GAACAAGACAAACAGTATGGACACAATTTATTTAAATGGAGAAAATTTTGTGTATACA 417





OTHER INFORMATION: Cys3Bb1 variant 11231nmv1  
US-11-192-801-18

## Alignment Scores:

Pred. No.:	2,63e-45	Length:	653
Score:	683.00	Matches:	207
Percent Similarity:	44.58%	Conservative:	122
Best Local Similarity:	28.05%	Mismatches:	283
Query Match:	17.34%	Indels:	126
	7	Gaps:	28

US-10-782-570-1 (1-2235) x US-11-192-801-18 (1-653)

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QY 4 AATCAAAATAATAATAAGTAATATGAGATTTCGATTCAAAGAATTTATCTTATCTCTCT 63
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 AACAGAAATATTGATCATCTAGATACCCCTTACACAAATAATCCAAATCAACCAATTACAA 123
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 20 GluLeuGlnThrAenHieAenGlnTyrProLeuAlaAspAenProAenSerThrLeuGlu 39
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 AACCAAAATTAACAAGAGTGGCTCAATATGTGTCAA---GGGAATACAAATATGGTGAT 180
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 40 GluLeuAenTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeuAsp 59
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 AATTTTCGAGACATTTGCTAGTCTGATACAAATGGCT---GCAGTTAGTGCAGGTACTATT 237
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 60 Aen-----SerThrValLysAspAlaValGlyThrGlyIleSer 72
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCCGATAGGA 297
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 73 ValValGlyGlnIleLeuGlyValValGly-----ValPro 84
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 298 ATAATAGTGCTATTAATAATATCTTTTGGTACCCTAATCACTGTCTTTGGCCCGGGA 357
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 85 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAenThrIleTrpProSer--- 103
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 358 GAACAAGCAAAACAGTAGTGACACAAATTTATAAATGGGAGAAATTTTGGTTCATACA 417
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 104 -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAspLys 121
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 418 CCGTTAACAGAAAGCATAAACAGCTAAAGTTTACAACTTTTGAAGAGGATTTAGACAAATA 477
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAenAen 141
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 478 TTACAAGCTATAATACAGCATAGATGATTCGGAGAAATTTAAAGACTACAAGCTCT 537
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 142 PheGluAspTyrValAenAlaLeuAenSerTrpLysLys----- 154
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 538 GGATTTACCACCATCATCAGCATTAACAACAGCTGCTTGAACCTTAAATAACAGTTGAG 597
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 155 ---ThrProLeuSerLeuArgSerLysArgSerGlnGlyArgIleArgGluLeuPheSer 173
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 598 AATGTTCAATGATTTTATTCGAGAAATPACCTGGTTTCCAACTTGAACCTTATAAAGC 657
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 174 GlnAlaGluSerHiePheArgAenSerMetProSerPheAlaValSerLysPheGluVal 193
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 658 CTATTACTACCTATTATTCGCAAGCTGCTAATTTTCAATTTTAAATTTTATTAACAAGGT 717
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 194 LeuPheLeuProThrTyrAlaGlnAlaAenThrHieLeuLeuLeuLysAspAla 213
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 718 GCTGAATGGCTGATGAATGAATGATCAGATATACATCTCTTCCAAATGAACCTAATGCT 777
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 214 GlnValPheGlyGluGlnTrpGlyLys----- 222
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 778 GGAACATCAGATGAC-----TATTATAAATCTTTTAAAGAAATAATACCTAAATAT 828
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 223 ---SerSerGluAspValAlaGluPheTyrArgGlnLeuLysLeuThrGlnGlnTyr 241
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 829 AGTAACATATTGTGCAATACCTATATAGAGAGGACTAAATAAATCTTGAAACGAACTAAT 888
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 242 ThrAspHieCysValAenTrpTyrAenValGlyLeuAenGlyLeuArgLysSerThrTyr 261
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 889 ATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 948
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 262 AspAlaTrpValLysPheAenArgPheArgArgGluMetThrLeuThrValLeuAspLeu 281
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 949 ATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTCATAGGAAGAATAGGT 1008
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 282 IleValLeuPheProPheTyrAspIleArgLeuTyrSerLys----- 295
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1009 GGCATTAAACCTGAACCTTACAAAGAGAAATTTATACAACTGAAATATAATTTTGACCGCTCT 1068
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 296 GlyValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheLeuLeuThr 314
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1069 ACTTACCTTGAATTCACCCCAATCTCGCTATAATGGAATATAATTTAACACGTCAGGG 1128
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 ThrLeuGlnLysTyrGlyProThrPheLeuSerIleGluAenSerIleArgLysPro--- 333
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1129 CTTAGATTATTTTCAATTTTATAGTGAATCTATATATTTATACAAA----- 1173
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 ---HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuArgProGlyTyr 352
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1174 -----AATGAAACGTPACCGGAATCGTTTGTAGTTGGTATTCGGAATCGT 1215
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 353 PheGlyLysAspSerPheAenTyrTrpSerGlyAenTyr-----ValGluThrArg 369
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1216 AATAGATCTACTTATGTACGACGAGAACTGAAATTTATATATGGAAGAAGAACAGGTCCA 1275
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 370 ProSerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGlu 389
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1276 CCCAACAAACCTTTAATACCAATTTGAATCCCTATAAAGTTTCAATTTGTAACGTATGA 1335
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 ProValGlnLys-----LeuSerPheAspGlyGlnLysValTyr---Arg 403
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1336 CAAGTA-----ACTCCTACTTCCCTTTCCTAAC-----ATATACCTTTACAATTAAT 1383
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 404 ThrIleAlaAenThrAspValAlaAlaTrpProAenGlyLysValTyrLeuGlyValThr 423
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1384 CAATTTGAACCTTTATTTAAATAAATTCACCTAGTATAATAATTA-----ACATATTCA 1434
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 LysValAspPheSerGlnTyrAspAspGlnLysAenGluThrSerThrGlnThrTyrAsp 443
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1435 GCT-----GGGGGAATTTTCTAATGATATAAATAAACAACCTGATTTTCAATTTCT 1485
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 444 SerLysArgAenAenGlyHisValSerAlaGlnAspSerIleAsp-----GlnLeuPro 461
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1486 GTAAAAAAGACTGTAAACCAATTTATTAATCCAAATTTGTTTACCAAGCTATAATAGTTAT 1545
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 462 ProGluThrThrAspGluProLeu-----GluLysAlaTyr 473
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1546 AGTCATATTTTATCCAGTTTCTTTTATTTTATTTCTTATATCTTATAAATTTGGATTAGCGCTA 1605
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 474 SerHisGlnLeuAenTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle--- 492
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1606 AATATTATTATATACAGGTGCATTAGATGGACACACAGTAGTGTGTTAATAAGAAATATGCA 1665
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 493 ---ProPhePheThr-----TrpThrHisArgSerValAspPhePheAenThr 507
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1666 ATATCAGATATAAATAATTTACATGATCCAGCAATCAAAGGTAAACAGCTCTGATACAAAC 1725
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 508 IleAspAlaGluLysIleThrGlnLeuProValValLysAlaTyrAlaLeuSerSerGly 527
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1726 TCTAAGTAAATGAGAGACCTGGTGCATACAGAGAGAACTTGGTTTATTATTAACA----- 1779
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 528 AlaSerIleIleGluGlyProGlyPheThrGlyGlyAenLeuLeuPheLeuLysGluSer 547
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1780 -----ATCAAGGGCGTTTAGAATTCATGATAGACTCTTAATTTCTACACAATCTTAT 1833
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 548 SerAenSerIleAlaLysPheLysValThrLeuAenSerAlaAlaLeuLeuGlnArgTyr 567
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1834 TACATTAGCTTCGTAGTACCTACAAATGGTGTGGAATATCTCTTCTTAATATATCTCTT 1893
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 568 ArgValArgIleArgTyrAlaSerThr-----ThrAenLeuArgLeu 581
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1894 ACAATACCGAGTAGTAATAGGAATACCACTCAACGACTCAACACACTTTTCTGTGTACA 1953
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      582 PheVal-----GlnAsnSerAsnAsnAspPheLeuValIle 593
Qy      1954 AATTATAAT-----AATTACAATACGGAGATTTTGGGTATTTC 1992
Db      594 TyrIleAsnLysThrMetAsnLysAspAspLeuThrTyrGlnThrPheAspLeuAla 613
Qy      1993 CAATTTCCAAGTACAGTACATTACCTTTAAATCGAAACATACCATTTATATTAATCGT 2052
Db      614 ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuIleGlyAlaGlu 633
Qy      2053 GCAGATGTATCAAAATTTCAATTTTAAATCATGATAAAATTTGAATTTATACCAAT 2106
Db      634 SerPheValSerAsnGluLysIleTyrIleAspLysIleGluPheIleProVal 651

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## RESULT 15

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US-11-192-801-20
; Sequence 20, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PRT
; LOCATION: (1)..(653)
; OTHER INFORMATION: Cry3BB1 variant 11231mv1
US-11-192-801-20

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Alignment Scores:
Pred. No.:      2,63e-45      Length:      653
Score:          683.00      Matches:      207
Percent Similarity: 44.58%      Conservative: 122
Best Local Similarity: 28.05%      Mismatches: 283
Query Match:      17.34%      Indels:      126
DB:              7          Gaps:      28

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US-10-782-570-1 (1-2235) x US-11-192-801-20 (1-653)

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Qy      4 AATCAAAATATATATGAATATGAGATTATCGATTCAAGAATTTATCTTATCTCTCT 63
Db      3 AsnProAsnAsnArgSerGluHieAspThrIle-----LysValThrProAsnSer 19
Qy      64 AACGAAATATTGATCTTCTAGATACCTTTACACAAATATCCAAATCAACCATTAACAA 123
Db      20 GluLeuGlnThrAsnHieAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39
Qy      124 AACCAAAATTAACAAGAGTGGCTCAATATGTGTCAA---GGGAATACAAATATGGTGTAT 180
Db      40 GluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeuAsp 59
Qy      181 AATTTCGAGACATTTGCTAGTGTGCTGATACAAATTCGT---GCAGTTAGTGCAGGTACTATT 237
Db      60 Asn-----SerThrValLysAspAlaValGlyThrGlyIleSer 72
Qy      238 GTATCCGGTACTCTGTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCATAGGA 297
Db      73 ValValGlyGlnIleLeuGlyValValGly-----ValPro 84
Qy      298 ATAATAGTGTCTATAATAATATCTTTTGGTACCCCTAATCACTGTCTTTGGCCCGCGGA 357

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Db      85 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTyrProSer--- 103
Qy      358 GAACAGACAAAAACAGTATCGACACAAATTTATTAAATGGGAGAAATTTTGGTGTATACA 417
Db      104 -----AspAlaAspProTyrLysAlaPheMetAlaGlnValGluValLeuIleAspLys 121
Qy      418 CCGTTACACAGAAACATAAACACAGCTAAAGTTACAACTTTAGAGAGATTAGACAAATA 477
Db      122 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 141
Qy      478 TTACAAAGCTATATAATCAGCATTAGATGATTGGAGAAAAATTTAAAAAGACTACAAGCTCCT 537
Db      142 PheGluAspTyrValAsnAlaLeuAsnSerTyrLysLys----- 154
Qy      538 GGATTACACCATCATCAGCATTTACAACAAGCTGCTTGTGACTCTTAAATACGATTTGAG 597
Db      155 ---ThrProLeuSerLeuArgSerLysArgSerGlnGlyArgIleArgGluLeuPheSer 173
Qy      598 AATGTTCCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAAGC 657
Db      174 GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 193
Qy      658 CTATTACTACTATTATTCGCAAGCTGCTAAATTTTCATTTAAATTTATTACACAAGGT 717
Db      194 LeuPheLeuProThrTyrAlaGlnAlaAsnThrHisLeuLeuLeuLeuLysAspAla 213
Qy      718 GCTGAATGCTGATGAATGCAATGCAGATATACATCTCTCACAATTTGAACCTTAATGCT 777
Db      214 GlnValPheGlyGluGluTyrGlyTyr----- 222
Qy      778 GGAACATCATGAC-----TATTATAAACTTTTAAAGAAATATATACCTAAATAT 828
Db      223 ---SerSerGluAspValAlaGluPheTyrArgArgGlnLeuLysLeuThrGlnGlnTyr 241
Qy      829 AGTAACTATTGTGCAAAATACCTATAGAGAGAGACTAAATAAACTTCGAAACGAACTAAT 888
Db      242 ThrAspHisCysValAsnTyrTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyr 261
Qy      889 ATGAGATGGAGTATATTATTAATGATTATCGAAGATATATGACTATTACTGTATTAGACT 948
Db      262 AspAlaTyrValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeu 281
Qy      949 ATCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATCAATAGGAAGAAATAGGT 1008
Db      282 IleValLeuPheProPheTyrAspIleArgLeuTyrSerLys----- 295
Qy      1009 GGCATTAAAACTGAACCTTACAAGAGAAATTTATACAACTGAAATATAATTTTGACCGCTT 1068
Db      296 GlyValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheLeuLeuThr 314
Qy      1069 ACTTACCTTGAATTCACCCCAATCTCGCTATATATGGAATATATATTAACACGTTCAAGG 1128
Db      315 ThrLeuGlnLysTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro--- 333
Qy      1129 CTTAGATATTATTTTATGATGAACCTTATATTTTATATACAAA----- 1173
Db      334 ---HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuArgProGlyTyr 352
Qy      1174 -----AATGAAACGTACGGAATCGTTTAGTTGTATTTGCGAATCGT 1215
Db      353 PheGlyLysAspSerPheAsnTyrTyrSerGlyAsnTyr-----ValGluThrArg 369
Qy      1216 AATAGATCTATTATGCTACGACGAGAACTGAAATTTATATATATGAGAGAAACACAGGTCCA 1275
Db      370 ProSerIleGlySerLysThrIleThrSerProPheTyrGlyAspLysSerThrGlu 389
Qy      1276 CCACAACAAAACTTTAATACCATTTGAATCTCTATAAAGTTTCAATTGTGAACGTATAGA 1335
Db      390 ProValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg 403
Qy      1336 CAAGTA-----ACTCTACTCTCCCTTTTCTTAAC-----ATATATCTTTTACAATTAAT 1383
Db      404 ThrIleAlaAsnThrAspValAlaAlaTyrProAsnGlyLysValTyrLeuGlyValThr 423

```

```
QY 1384 CAAATTGAACCTTTATTTAAATAAATTCACCTAGTAATAAATA-----ACATATTCA 1434
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
424 LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp 443
QY 1435 GCT-----GGGGGGAATTTATCTAATGATAAAAAACAACGTGATTTTCAATTTCTT 1485
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
444 SerLysArgAsnAsnGlyHisValSerAlaGlnAspSerIleAsp-----GlnLeuPro 461
QY 1486 GTAAAAAAGACTGTAAACCAATTATTATCCAAATGTTTACCAGCTATAATAGTTAT 1545
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
462 ProGluThrThrAspGluProLeu-----GluLysAlaTyr 473
QY 1546 AGTCATATTTTATCCAGCTTTTCTTTTATTAAATTCTCTATAAAATTTGGATTAGCGCTA 1605
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
474 SerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle--- 492
QY 1606 AATATATTATATACAGGTGCATTAGGATGGACACACAGTAGTGTGTTAAAGAAATAATGCA 1665
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
493 ---ProPhePheThr-----TrpThrHisArgSerValAspPhePheAsnThr 507
QY 1666 ATATCAGATAAAATAATTAATGATGCCAGCAATCAAAGGTAAACAGTCTTGATACAAC 1725
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
508 IleAspAlaGluLysIleThrGlnLeuProValValLysAlaTyrAlaLeuSerSerGly 527
QY 1726 TCTAAGGTAAATTGAAGGACCTGTCATACAGGAGAACTTGGTTTATTATCAA----- 1779
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
528 AlaSerIleIleGluGlyProGlyPheThrGlyGlyAsnLeuLeuPheLeuLysGluSer 547
QY 1780 -----AGTCAAGGCGGTTTAGAGATTACATGTAGAACTCCTTAATTTACACAATCTTAT 1833
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
548 SerAsnSerIleAlaLysPheLysValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyr 567
QY 1834 TACATTAGACTTCGATACGCTACAATGGTGTGGAAATACTCTTCCTTAATATATCTCTT 1893
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
568 ArgValArgIleArgTyrAlaSerThr-----ThrAsnLeuArgLeu 581
QY 1894 ACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACACACTTTTCTCGGTACA 1953
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
582 PheVal-----GlnAsnSerAsnAsnAspPheLeuValIle 593
QY 1954 AATTATAAT-----AATTACAATACGAGATTTTGGGTATTTC 1992
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
594 TyrIleAsnLysThrMetAsnLysAspAspLeuThrTyrGlnThrPheAspLeuAla 613
QY 1993 CAATTCCAGTACAGTACATTACCTTTAAATCGAAACATACCATTTATATTATTCGT 2052
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
614 ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeuIleIleGlyAlaGlu 633
QY 2053 GCAGATGTATCAATTTCAATTTTAAATTCATGATAAAATTTGAATTTATACCAATT 2106
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
634 SerPheValSerAsnGluLysIleTyrIleAspLysIleGluPheIleProVal 651
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Search completed: January 12, 2006, 06:43:15

Job time : 55 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 12, 2006, 06:18:19 ; Search time 43 Seconds  
(without alignments)  
8594.425 Million cell updates/sec

Title: US-10-782-570-1

Perfect score: 3939

Sequence: 1 gtgaatcaaaataataa.....caaatatgatattgattaa 2235

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -n2p.model -DEV=xlpl  
-Q=/cgn2\_1/USPTO\_spool\_p/US10782570/runat\_12012006\_060222\_7551/app\_query.fasta\_1.2375  
-DB=Issued Patents AA -QFMT=fastran -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10782570@cgn\_1\_1\_50@runat\_12012006\_060222\_7551 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:

1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1153	29.3	1180	2	US-09-224-024-28
2	1153	29.3	1180	4	PCT-US94-07902-28
3	900	22.8	686	2	US-09-224-024-31
4	900	22.8	686	4	PCT-US94-07902-31
5	787.5	20.0	1169	1	US-08-315-468-4
6	706	17.9	651	1	US-08-315-468-6
7	706	17.9	651	2	US-07-941-650A-4
8	706	17.9	659	2	US-08-996-441B-112
9	706	17.9	659	2	US-08-993-722A-112
10	706	17.9	659	2	US-08-993-170A-112
11	706	17.9	659	2	US-08-993-775B-112
12	706	17.9	659	2	US-09-427-770-112

13	706	17.9	659	2	US-09-427-769-112	Sequence 112, App
14	700	17.8	652	2	US-08-996-441B-110	Sequence 110, App
15	700	17.8	652	2	US-08-993-722A-110	Sequence 110, App
16	700	17.8	652	2	US-08-993-170A-110	Sequence 110, App
17	700	17.8	652	2	US-08-993-775B-110	Sequence 110, App
18	700	17.8	652	2	US-09-377-466B-4	Sequence 4, Appli
19	700	17.8	652	2	US-09-427-770-110	Sequence 110, App
20	700	17.8	652	2	US-09-427-769-110	Sequence 110, App
21	700	17.8	652	2	US-10-232-665-4	Sequence 4, Appli
22	700	17.8	652	4	PCT-US92-00040-2	Sequence 2, Appli
23	693	17.6	652	2	US-09-377-466B-6	Sequence 6, Appli
24	693	17.6	652	2	US-10-232-665-6	Sequence 6, Appli
25	691	17.5	652	2	US-08-996-441B-4	Sequence 4, Appli
26	691	17.5	652	2	US-08-996-441B-10	Sequence 10, Appl
27	691	17.5	652	2	US-08-996-441B-28	Sequence 28, Appl
28	691	17.5	652	2	US-08-996-441B-44	Sequence 44, Appl
29	691	17.5	652	2	US-08-996-441B-68	Sequence 68, Appl
30	691	17.5	652	2	US-08-996-441B-98	Sequence 98, Appl
31	691	17.5	652	2	US-08-996-441B-111	Sequence 111, App
32	691	17.5	652	2	US-08-993-722A-4	Sequence 4, Appli
33	691	17.5	652	2	US-08-993-722A-10	Sequence 10, Appl
34	691	17.5	652	2	US-08-993-722A-28	Sequence 28, Appl
35	691	17.5	652	2	US-08-993-722A-44	Sequence 44, Appl
36	691	17.5	652	2	US-08-993-722A-68	Sequence 68, Appl
37	691	17.5	652	2	US-08-993-722A-98	Sequence 98, Appl
38	691	17.5	652	2	US-08-993-722A-111	Sequence 111, App
39	691	17.5	652	2	US-08-993-170A-4	Sequence 4, Appli
40	691	17.5	652	2	US-08-993-170A-10	Sequence 10, Appl
41	691	17.5	652	2	US-08-993-170A-28	Sequence 28, Appl
42	691	17.5	652	2	US-08-993-170A-44	Sequence 44, Appl
43	691	17.5	652	2	US-08-993-170A-68	Sequence 68, Appl
44	691	17.5	652	2	US-08-993-170A-98	Sequence 98, Appl
45	691	17.5	652	2	US-08-993-170A-111	Sequence 111, App

## ALIGNMENTS

### RESULT 1

US-09-224-024-28  
; Sequence 28, Application US/09224024  
; Patent No. 6056953  
; GENERAL INFORMATION:  
; APPLICANT: Lesliie Hickie  
; APPLICANT: Jewel Payne  
; TITLE OF INVENTION: Materials and Methods for the Control of  
; TITLE OF INVENTION: Calliphoridae Pests  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/224,024  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/956,226  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA79  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800



QY	1879	CCTAATATATCTCTTCAATACACGAGTAATAGGAATACCACCTCAACGACTCAACAAC	1938
DB	602	AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro	620
QY	1939	ACTTTTCTGGTACAAATTAATAATTTACATACGGAGATTTTGGGTATTTCCAAATTT	1998
DB	621	ThrPheSerGlyThrAspTyThrAsnLeuLysTyLysAspGheGlnTyLeuGluPhe	640
QY	1999	CCAAGTACAGTAAACATTTACCTTTTAAATCGAAACATACCAATATATATTTAATCGTCGAGAT	2058
DB	641	SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp	660
QY	2059	GTA---TCAAAATTCAAATTTAATCATTTGATAAAATTTGAATTTATACCAATTACTCTCTCT	2115
DB	661	ValTyThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer	680
QY	2116	GTACGCCAAATAGAGAAAAACAAAATTAGAAACTATCCAAACAAAAATAATACATTT	2175
DB	681	IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleIleAsnThrPhe	700
QY	2176	TTCACAAAATCATACAAAAATATCTTTAAATATATAGAGCCCAAAACTATGATATGTAT	2232
DB	701	TyrAlaAsnProIleLysAsnThrLeuGlnIleSerGluLeuThrAspTyLysAspIleAsp	719

Pred. No.:	3.98e-96	Length:	1180
Score:	1153.00	Matches:	282
Percent Similarity:	54.41%	Conservative:	131
Best Local Similarity:	37.15%	Mismatches:	282
Query Match:	29.27%	Indels:	64
DB:	4	Gaps:	25

US-10-782-570-1 (1-2235) x PCT-US94-07902-28 (1-1180)

Qy	13	AATAAATAATGAATATGAGATTATCGATTCA-----AAGAATTTATCTTATCTTCTTAAC	66
Db	6	AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnLysSerAsnAsn	25
Qy	67	AGAAATATGATCAATCTTAGATACCCCTTACACAAATAATCCAAATCAACCAATTACAAAC	126
Db	26	-----TyrThrArgTyrProIleGluAsnSerProLysGlnLeuLeuGlnSer	41
Qy	127	ACAAATTTACAAAGAGTGGCTCAATATCTGTCAAGGAATACACAATATGGTGATAATTTC	186
Db	42	ThrAsnTyrLysAspTyrLysAsnMetCysGlnGlnAsnGlnGlnTyrGlyLysPhe	61
Qy	187	GAGACATTTGCTAGTGTGCTATACAAATTTGTCAGTTAGTCAGGTACTATTGTATCCGGT	246
Db	62	GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValValGly	78
Qy	247	ACTCTGTTAGCCGGTATAGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGGT	306
Db	79	ThrValLeuThrGlyPheGlyPheThr-----ProLeuGlyLeu-----	92
Qy	307	GCTATATATATCTTTTGGTACCTTAATCACTGCTCTTTTGGCCGGCGGAGAACACAGC	366
Db	93	---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer	111
Qy	367	AAAACGATGGACACAAATTTATTAATAATGGAGAAATTTTGTGTGATACACCGTTTACA	426
Db	112	AsnThr---TrpSerAspPheIleThrGlnThrLysAsnLleIleLysLysGluIleAla	130
Qy	427	GAAGACATAAACACAGCTAAAGTTTACAACCTTTAGAGGATTTTGACAAATATTACAAAGC	486
Db	131	SerThrTyrIleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr	150
Qy	487	TATATATACAGCATTAGATGATTGGAGAAATTAATAAGACTACAAAGCTCCCTGGATTACCA	546
Db	151	TyrHisAsnHisLeuLysThrTrpGlu-----AsnAsnProAsnProGln	165
Qy	547	CCATCATCAGCATTAACAACAGCTGCTTGACTCTTAAATACGATTTGAGAATGTTCCAC	606
Db	166	AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle	185
Qy	607	AATGATTTTATTCGAGAATACTT-----GGTTTCCAACCTTGAAACCTTATAAACGCTTA	660
Db	186	ProGluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu	205
Qy	661	TTACTACCTATTATGTCGCAAGCTGCTTAATTTTCAATTTATTTATTAACAACAGGTGCT	720
Db	206	ValLeuSerSerTyrAlaGlnAlaAlaAsnLeuHisIleuThrValLeuAsnGlnAlaVal	225
Qy	721	GAATTGGCTGATGAATGGAATGCAGATATACATCCTTACAAATGAACCTTAATGCTGGA	780
Db	226	LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro	244
Qy	781	ACATCAGATGACTATTATAAATTTTAAAGAAAATATACCTAAATATATAGTAACCTATTGT	840
Db	245	ThrAlaIleAspTyrTyrProValLeuThrLysAlaIleGluAspTyrThrAsnTyrCys	264
Qy	841	GCAATACCTTATAGAGAAGGACTAAATAACTCTGAAACGACCTT-----	885
Db	265	ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp	284
Qy	886	---AATATGAGATCGAGCTATATTAAATGATTATCGAAGATATATGCTACTATTCTATTATTA	942
Db	285	GlyAsnIleAsnTrpAsnThrTyrAsnThrTyrArgThrLysMetThrAlaValLeu	304



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::: ||| |||::: |||::: |||::: |||
Db 641 SerAsnGluValIysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660

Qy 2059 GTA---TCAAATTCAAATTTTAATCAATGATAAAATTTGAATTTATACCAATTTACTTCCTCT 2115
::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680

Qy 2116 GTACGCCAAATAGAGAAAAACAAAATTAGAAACTATCCAAACAAAATAAAATACATTT 2175
::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 681 IleArgGluAspArgGluLysGlnLysLeuGluThrValGlnGlnIleAsnThrPhe 700

Qy 2176 TTCACAAATCATACAAAAATACTTTTAAATATATAGAGCCCAAACTATGATATTTGAT 2232
::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db 701 TyrAlaAsnProIleLysAsnThrLeuGlnSerGluLeuThrAspTyrAspIleAsp 719

RESULT 3
US-09-224-024-31
; Sequence 31, Application US/09224024
; Patent No. 6056953
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Leslie Hickie
; TITLE OF INVENTION: Materials and Methods for the Control of
; TITLE OF INVENTION: Calliphoridae Pests
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-224-024-31

Alignment Scores:
Pred. No.: 3,25e-73 Length: 686
Score: 900.00 Matches: 251
Percent Similarity: 48.03% Conservative: 115
Best Local Similarity: 32.94% Mismatches: 268
Query Match: 22.85% Indels: 128
DB: 2 Gaps: 32

US-10-782-570-1 (1-2235) x US-09-224-024-31 (1-686)

Qy 13 AATAATAATGAATATGAGATATATCGAATTCAGAAATTTATCTTATCTCTTAACAGAAAT 72
Db 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25

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Db 655 AspTyrThrGluLeuGlnAsnIleGluLeuThrGlnLysIleValAsnAspLeuPheVal 674  
Qy 2182 AATCAT 2187  
Db 675 AsnAsn 676

RESULT 4  
PCT-US94-07902-31  
; Sequence 31, Application PC/TUS9407902  
; GENERAL INFORMATION:  
; APPLICANT: Street address: 4980 Carroll Canyon Road  
; APPLICANT: City: San Diego  
; APPLICANT: State/Province: California  
; APPLICANT: Country: US  
; APPLICANT: Postal code/Zip: 92121  
; APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991  
; APPLICANT: Telex number:  
; TITLE OF INVENTION: Materials and Methods for the Control of  
; TITLE OF INVENTION: Calliphoridae Pests  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: PCT/US94/07902  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA79  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 686 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US94-07902-31

Alignment Scores:  
Pred. No.: 3.25e-73 Length: 686  
Score: 900.00 Matches: 251  
Percent Similarity: 48.03% Conservatve: 115  
Best Local Similarity: 32.94% Mismatches: 268  
Query Match: 22.85% Indels: 128  
DB: 4 Gaps: 32

US-10-782-570-1 (1-2235) x PCT-US94-07902-31 (1-686)

Qy 13 AATAATATGATATGAGATTATCGATTCAAGAAATTTATCTTATCTTCAACAGAAAT 72  
Db 6 AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn 25  
Qy 73 ATTGATCATCTTAGATACCTTACACAATATCCAAATCAACCATACCAAAACACAAAT 132  
Db 26 -----TyrSerArgTyrProLeuAlaAsnLysProAsnGlnProLeuLysAsnThrAsn 43  
Qy 133 TACAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATAATTTTCGAGACA 192

Db 44 TyrLysAspTrpLeuAsnValCysGlnAspAsnGlnGlnTyrGlyAsnAsnAlaGlyAsn 63  
Qy 193 TTTGCTAGTCTGATACAAATGCTGCAGTTAGTCAGGTACTATTGTATCCGGTACTCTG 252  
Db 64 PheValSerSerGluThrIleValGlyValSerAlaGlyIleIleValValGlyThrMet 83  
Qy 253 TTAGCCGGTATAGTGGGCTCACTTCTATATCCGACCGATAGGAATAAATAGGTGCTATA 312  
Db 84 LeuGly-----AlaPheAlaAlaPro-----ValLeuAlaAlaGly 95  
Qy 313 ATAATATCTTTTGGTACCTTAATCAGTCTCTTTTGGCCCGCGGAGAACAGACAAACA 372  
Db 96 IleIleSerPheGlyThrLeuLeuProIlePheTrp---GlnGlySerAspProAlaAsn 114  
Qy 373 GTATGGACACAATTTATTAATAATGGGAGAAATTTTGTGTATACACCGTTAAACAGAA--- 429  
Db 115 ValTrpGlnAspLeuLeuAsnIleGly-----GlyArgProIleGlnGluIle 130  
Qy 430 -----AGCATAAACACAGCTAAAGTTTACAAACTTTAGAGGATTTAGACAAATATTACAA 483  
Db 131 AspLysAsnIleIleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp 150  
Qy 484 AGCTATAATACAGCATTTAGATGATTGGAGAAATTTAAAGAGACTACAAAGCTCTCTGGATTA 543  
Db 151 LysTyrGlnGluPhePheAspLysTrpGluProAlaArg----- 163  
Qy 544 CCACCATCATCAGCATTAACAACAGCTGCTTAAATACGATTTAAATACGATTTGAGAATGTT 603  
Db 164 -----ThrHisAlaAsnAlaLysAlaValLHisAspLeuPheThrThrLeuGluProIle 181  
Qy 604 CACAAT-----GATTTTATTCGAGAAATACCTGTTTCCAACTTGAACCTTATAAA 654  
Db 182 IleAspLysAspLeuAspMetLeuLysAsnAlaSerTyrArgIleProThr----- 199  
Qy 655 ACGCTATTACTACTATTATGCGCAAGCTGTAATTTTCATTTTAAATTTTATTACAAACA 714  
Db 200 -----LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis 216  
Qy 715 GTGTGTAATTTGGCTGATGAATGGAATGCAGATATACATCTCTCACAAATTTGAACCTAAT 774  
Db 217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyIleAsnProSer 233  
Qy 775 GCTGGAACATCAGATGACTATTATAA---CTTTTAAAGAAATATACCTTAAATATAGT 831  
Db 234 ThrPheAsnSerSerAsenTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr 253  
Qy 832 AACTATTGTGCAAAATACCTATAGAGAGAGACTAAATAAACTTCGAAACGAACTTAATATG 891  
Db 254 AspTyrCysIleGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273  
Qy 892 AGATGGAGTATATTATGATGATATCGAGATATATGACTATTACTGTATTAGATCTATC 951  
Db 274 ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293  
Qy 952 GCTCAATTTTCTTTTATGATATAAGAGATACAAAGATTCAAATGAGGAAGTAATAGGTGGC 1011  
Db 294 AlaIlePheProAsnTyrAspProGluLysTyrProIle-----Gly 307  
Qy 1012 ATTAAACTGAACCTTACAAGAGAAATTTATACAACTCGAAATAAATTTTGACCGCTTACT 1071  
Db 308 ValLysSerGluLeuThrArgGluValTyr---ThrAsnValAsnSerAspThrPheArg 326  
Qy 1072 TACCTTGAATTCACCCCAATCTCGCTATATGATATGATATTAATTTAAACAGTTCAGGCGTT 1131  
Db 327 -----ThrIleThrGluLeuGluAsnGlyLeuThrArgAsnPro--- 339  
Qy 1132 AGATTATTTTTCATTTTATGATGAACCTTATATTTTATACAAAAAT----- 1176  
Db 340 ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359  
Qy 1177 GAAACGCTAC-----GGGAATCGTTTGTGTTAGTTGCTATTTGCGAATCGTAAT 1218  
Db 1177 GAAACGCTAC-----GGGAATCGTTTGTGTTAGTTGCTATTTGCGAATCGTAAT 1218







[illegible]

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Qy 1987 TAT-----TTCAAAATTTCAGTACAGTAAACATTACCTTTAAATCGAACAATACCATTTT 2040
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Db 606 TyrGlnThrPheAspGluAlaThrSer-----AsnSerAsnMetGlyPhe 620
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 2041 ATATTTAATCGTGCAGAT-----GATCAAAATTTCAAATTTTA 2076
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 621 SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 640
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 2077 ATCATTGATAAATTTGAATTTATACCAATTT 2106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 641 TyrIleAspLysIleGluPheIleProVal 650
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RESULT 7
US-07-941-650A-4
; Sequence 4, Application US/07941650A
; Patent No. 6294184
; GENERAL INFORMATION:
; APPLICANT: Uyeda, Kendrick A.
; APPLICANT: Bradfisch, Gregory A.
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/941,650A
; FILING DATE: 19920908
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,020
; FILING DATE: 12-SEP-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/658,935
; FILING DATE: 21-FEB-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,112
; FILING DATE: 16-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: tolworthi
; INDIVIDUAL ISOLATE: 43f
; IMMEDIATE SOURCE:
; CLONE: E. coli XL1-Blue (pML98-4), NRRL B-18291
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..651
; US-07-941-650A-4

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## Alignment Scores:

Pred. No.: 1.37e-55 Length: 651  
Score: 706.00 Matches: 216  
Percent Similarity: 44.27% Conservative: 116  
Best Local Similarity: 28.80% Mismatches: 270  
Query Match: 17.92% Indels: 148  
DB: 2 Gaps: 31

US-10-782-570-1 (1-2235) x US-07-941-650A-4 (1-651)

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QY 1 GTGAATCAAAATATAAATAAGTATGAGATATCGAT-----TCAAAGATTTATCTTAT 57
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QY 58 CTTCTTAACAGAAATATTGATCATTTCTAGATACCTTACACAAATAATCCAAATCAACA 117
DB 21 ProThrAen-----HisAenGlnTyrProLeuAlaAaspAasnProAasnSerThr 36
QY 118 TTCAAAAACACAAATTTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAAATATG 177
DB 37 LeuGluGluLeuAenTyrLysGluPheLeuArgMetThrAlaAaspAasnSerThr----- 54
QY 178 GATAATTCGACAAATTTGCTAGTCTGCTGATACAAATGCTGCGAGTTAGTGCAGGTACTATT 237
DB 55 -----GluValLeuAaspSerSerThrValLysAaspAlaValGlyThrGlyIleSer 71
QY 238 GTATCCGGTACTGTTAGCCGGTATAGTGGCTCACTTCTATATCCGGACCGATAGGA 297
DB 72 ValValGlyGlnIleLeuGlyValValGly-----ValPro 83
QY 298 ATAATAGTGTCTATAATAATCTTTTGGTACCCCTAATCACTGTCTTTTGGCCCGCGGA 357
DB 84 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAenAlaIleTyrProSer--- 102
QY 358 GAACAAGACAAACAGTAGTAGACACAAATTTATAAATGGGAGAAATTTTGTGTGATACA 417
DB 103 -----AaspAaaspProTyrLysAlaPheMetAlaGlnValGluValLeuIleAaspLys 120
QY 418 CGGTAAACAGAAAGCATAAACAGCTAAAGTTACAACTTTTGAAGAGGATTTAGACAAATA 477
DB 121 LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAenAen 140
QY 478 TTCAAAAGCTATAATACAGCATTAGATGATGGAGAAATTAATAAGACTACAAGCTCT 537
DB 141 PheGluAaspTyrValAasnAlaLeuAaspSerTyrLysLys----- 153
QY 538 GGATTAACCAATCATCAGCATTAACAACAGCTGCTTGAATCTTTAAATACGATTTAG 597
DB 154 ---AlaProValAasnLeuAargSerArgSerGlnAaspArgIleAargGluLeuPheSer 172
QY 598 ATGTTCACATGATTTTATTCGAGNAATACCTGGTTTCCAACTTGAACCTTATAAAGC 657
DB 173 GlnAlaGluSerHisPheAasnSerMetProSerPheAlaValAserLysPheGluVal 192
QY 658 CTATTACTACTATTATTCGCAAGCTGCTTAATTTTCAATTTAAATTTTATTAACAAGGT 717
DB 193 LeuPheLeuProThrTyrAlaGlnAlaAasnThrHisLeuLeuLeuLeuLysAaspAla 212
QY 718 GCTGAATTCGGCTGATGAATGGAATGCAGATATACATCTTCTCAAAATTGAACCTAATGCT 777
DB 213 GlnValPheGlyGluGluTyrGlyTyr----- 221
QY 778 GGAACATCAGATGAC-----TATTATAACTTTTAAAGAAATATACCTAAATAT 828
DB 222 ---SerSerGluAaspIleAlaGluPheTyrGlnAargGlnLeuLysLeuThrGlnGlnTyr 240
QY 829 AGTAACATTTGTGCAATACCTATAGAGAGGACTAAATAAATCTCGAAACCAACCTAAT 888
DB 241 ThrAaspHisCysValAasnTyrAasnValGlyLeuAasnSerLeuAargGlySerThrTyr 260
QY 889 ATGAGATGGAGTATATTATTAATGATTATCGAAGATATATGACTATTATCTATTAGTACT 948
DB 261 AspAlaTyrValLysPheAasnArgPheArgGluMetThrLeuThrValLeuAaspLeu 280
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QY 949 ATCCGCTCAATTTCTTTTATGATATAAAGAGATACAAAGATTTCAATAGGAAGATAGGT 1008
DB 281 IleValLeuPheProPheTyrAaspValAargLeuTyrSerLys----- 294
QY 1009 GGCATTAATAAAGTCAACTTACAAAGAAATTTATCAACTGAAATTAATTTTACCGCTCTT 1068
DB 295 GlyValLysThrGluLeuThrArgAaspIlePheThrAaspProIle---PheThrLeuAen 313
QY 1069 ACTTACCTTGAATTTCAACCCCAATCTCGCTATAATGGAATATAATTTAAACAGTTTCAGG 1128
DB 314 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAenSerIleAargLysPro--- 332
QY 1129 CTTAGATTATTTTCAATTTTATAGATCAACTTATATTTATACAAA----- 1173
DB 333 ---HisLeuPheAaspTyrLeuAargGlyIleGluPheHisThrArgLeuAargProGlyTyr 351
QY 1174 -----AATGAACGTCACGGGAATCGTTTGTAGTTGGTATTTCGGAATCGT 1215
DB 352 SerGlyLysAaspSerPheAasnTyrTyrSerGlyAasnTyr-----ValGluThrArg 368
QY 1216 AATAGATCTACTTATGCTACGACAGAACTGAAATTTATATATGGAAGAAGACAGGTCCA 1275
DB 369 ProSerIleGlySerAasnAaspThrIleThrSerProPheTyrGlyAaspLysSerIleGlu 388
QY 1276 CCCCAACACAAAACTTTTAATACCATTTCAATCTTATAAAGTTTCAATTTGTAACGTATAGA 1335
DB 389 ProlIleGlnLys-----LeuSerPheAaspGlyGlnLysValTyr-----Arg 402
QY 1336 CAAGTA-----ACTCTACTTCCCTTTCTCTAAC-----ATATACTTTTACAATTAAT 1383
DB 403 ThrIleAlaAasnThrAaspIleAlaAaPheProAaspGlyLysIleTyrPheGlyValThr 422
QY 1384 CAATTTGAACCTTTATTTAAATAATTCACCTAGTAATAAATTA-----ACATATTCCA 1434
DB 423 LysValAaspPheSerGlnTyrAaspAaspGlnLysAenGluThrSerThrGlnThrTyrAasp 442
QY 1435 GCT-----GGGGGGAATTTTCTCTAATGATAAA-----AAA 1464
DB 443 SerLysAargTyrAasnGlyTyrLeuGlyAlaGlnAaspSerIleAaspGlnLeuProGlu 462
QY 1465 ACAACTGATTTTCAATTTCTGTGTAATAAAGACTGTAAACCAATTTAATTCACCAATTTGT 1524
DB 463 ThrThrAasp-----GluProLeuGluLys----- 470
QY 1525 TTACCAAGCTATATAGTTATAGTATCATATTTTATCCAGTTTCTTTTATTTAATTTATCC 1584
DB 471 -----AlaTyrSerHisGlnLeuAenTyrAlaGluCysPheLeuMetGln 485
QY 1585 TATAAAATTTGGATTAGCGCTAAATATATATATATACAGGTGCAATTAGGATGACACACAGT 1644
DB 486 AspAargAargGlyThrIle-----ProPhePheThr-----TyrThrHisAarg 499
QY 1645 AGTGTAAATAGAAATAATGCAATATCAGATAAATAATTAATATCAATGATCCCAAGATCAAA 1704
DB 500 SerValAaspPheAasnThrIleAaspAlaGluLysIleThrGlnLeuProValLys 519
QY 1705 GGTAACAGCTCTTGATACAACTCTAAGGTAAATGAAGGACCTGTGTCATACAGAGGAAAC 1764
DB 520 AlaTyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAen 539
QY 1765 TTGGTTTATTTTACAA-----AGTCAAGGGCGGTTTATAGAGTTATACATGTAAGTACT 1812
DB 540 LeuLeuPheLeuLysGluSerSerAasnSerIleAlaLysPheLysValThrLeuAenSer 559
QY 1813 CCTAATTTCTACAACTTATTTACATTTAGACTTTCGATTCGATCAAAATGGTGTGGAAT 1872
DB 560 AlaAlaLeuLeuGlnAargTyrArgValAargIleAargTyrAlaSerThr----- 575
QY 1873 ACTCTTCTCTATATATCTTTTACATATACAGAGGATTAATAGGAATACCACTCAACGCTC 1932
DB 576 -----ThrAasnLeuAargLeuPheVal-----GlnAasnSer 585
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Db      629  SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 649
Qy      2077 ATCATTTGATAAATTTGAATTTATACCAATT 2106
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Db      649  TyrIleAspLysIleGluPheIleProVal 658
          |||||||

RESULT 9
US-08-993-722A-112
; Sequence 112, Application US/08993722A
; Patent No. 6060594
; GENERAL INFORMATION:
; APPLICANT: English, Leigh H.
; APPLICANT: Brussock, Susan M.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Bryson, James W.
; APPLICANT: Kulesza, Caroline A.
; APPLICANT: Kulesza, Frederick S.
; APPLICANT: Slatin, Stephen L.
; APPLICANT: Von Terssch, Michael A.
; APPLICANT: Romano, Charles
; TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
; TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/993,722A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3106
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 659 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-993-722A-112

Alignment Scores:
Pred. NO.: 1.38e-55 Length: 659
Score: 706.00 Matches: 216
Percent Similarity: 44.27% Conservative: 116
Best Local Similarity: 28.80% Mismatches: 270
Query Match: 17.92% Indels: 148
DB: 2 Gaps: 31

US-10-782-570-1 (1-2235) x US-08-993-722A-112 (1-659)
Qy      1  GTGAATCAAAATATAATGAATATGAGATTATCGAT---TCAAGAAATTTATCTTAT 57
          : : : : : ||||| : : : : : ||||| : : : : : |||||
Db      9  MetAsnProAsnAsnArgSerGluTyrAspThrIleLysValThrProAsnSerGluLeu 28
          : : : : : ||||| : : : : : ||||| : : : : : |||||
Qy      58  CTTTCTTACAGAAATATTGATCTTCTAGATACCCCTTACACAAATTAATTCAAATCAACCA 117
          : : : : : ||||| : : : : : ||||| : : : : : |||||
Db      29  ProThrAsn-----HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr 44
          : : : : : ||||| : : : : : ||||| : : : : : |||||

Qy      118  TTACAAAACACAAATTACAAAGAGTGCGTCAATATGTGTCAAGGGGAATACACATATGGT 177

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[illegible]

Db	360	SerGlyLyAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg	376
Qy	1216	AATAGACTCTATTATGCTACGACGAGNACTGAAATTATATATATGAGAAAGAACAGGTCCA	1275
Db	377	ProSerIleGlySerAsnAspThrIleThrSerProPheTyrGlyAspYsserIleGlu	396
Qy	1276	CCCAACAACAAACTTTTAATACCAATTCCTATAAAGTTTCAATTGCTAACTGATGATA	1335
Db	397	ProIleGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg	410
Qy	1336	CAAGTA-----ACTCCTACTTCCCTTTTCCTAAC-----ATATACTTTTCAATAAT	1383
Db	411	ThrIleAlaAsnThrAspIleAlaAlaPheProAspGlyLysIleTyrPheGlyValThr	430
Qy	1384	CAAAATCGAACTTTATTTAAATAATTCACCTAGTAATAAATTA-----ACATATTCA	1434
Db	431	LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp	450
Qy	1435	GCT-----GGGGGAATTTATCTAATGATAAA-----AAA	1464
Db	451	SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProGlu	470
Qy	1465	ACAACTGATTTTCAATTTCTCGTAAAAAAGACTGTAAACCAATTATTATCCAAATGT	1524
Db	471	ThrThrAsp-----GluProLeuGlyLys-----	478
Qy	1525	TTACCAAGCTATAATAGTATAGTATCATATTTTATCCAGTTTCTTTATTATTATTC	1584
Db	479	-----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln	493
Qy	1585	TATAAAATTCGATTAGCGCTAAATATATTATATACAGGTGCATTAGGATGGACACACAGT	1644
Db	494	AspArgGlyThrIle-----ProPhePheThr-----TrpThrHisArg	507
Qy	1645	AGTGTTAATAGAATAATGCAATATCAGATAAAATAATACAAATGATCCAGCAATCAA	1704
Db	508	SerValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValValLys	527
Qy	1705	GGTAACAGTCTTGATACAACTCTAAGTAATTGAAGGACCTGGTCATACAGAGGAAC	1764
Db	528	AlaTyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsn	547
Qy	1765	TTGGTTTATTATTCACAA-----AGTCAAGGGCGTTTAGAGATTACATGTAGAACT	1812
Db	548	LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer	567
Qy	1813	CCTAATTCTACAACTTTATTATACACTTCGATACGCTACAAATGGTCTCGAAAT	1872
Db	568	AlaAlaLeuLeuGlnArgTyrArgValAlaGileArgTyrAlaSerThr-----	583
Qy	1873	ACTCTTCTTAATATATCTCTTACAAATCCAGGAGTAATAGGAATACCACCTCAACGCTC	1932
Db	584	-----ThrAsnLeuArgLeuPheVal-----GlnAsnSer	593
Qy	1933	AACAACACTTTTTCTGGTACAAATATATAATATTTACAATAC-----GGAGATTTTGGG	1986
Db	594	AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr	613
Qy	1987	TAT-----TTCCAAATTTCCAGTACAGTAACATTTACCTTTTAATTCGAAACATACAT	2040
Db	614	TyrGlnThrPheAspPheAlaThrSer-----AsnSerAsnMetGlyPhe	628
Qy	2041	ATATTTAATTCGTGCACAT-----GTATCAAAATCAATTTTA	2076
Db	629	SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle	648
Qy	2077	ATCATTGATAAAATGAATTTTATACCAATT	2106
Db	649	TyrIleAspLysIleGluPheIleProVal	658





Db 129 LysLeuGluGlyTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsn 148  
QY 478 TTACAAGCTATATACAGCATATGATGGAGAAATTAAGAGACTACAGCTCCT 537  
Db 149 PheGluAspTyrValAsnAlaLeuAspSerTrpLysLys----- 161  
QY 538 GGATACCACCATCATCAGCATACACAGCTGCTTGAATCTTTAAATACGATTGAG 597  
Db 162 ---AlaProValAsnLeuArgSerArgGlnAspArgGleArgGluLeuPheSer 180  
QY 598 AATGTTCAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTATAAAG 657  
Db 181 GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 200  
QY 658 CTATTACTACCTATTATTCGCAAGCTGCTAAATTTTCAATTTTAAATTTATTAACAAGGT 717  
Db 201 LeuPheLeuProThrTyrAlaGlnAlaAlaAsnThrHisLeuLeuLeuLysAspAla 220  
QY 718 GCTGAATTGGCTGATGAATGGAATGCAGATATACATCTTCAAAATTTGAACCTAATGCT 777  
Db 221 GlnValPheGlyGluGlyTrpGlyTyr----- 229  
QY 778 GGAACATCAGATGAC-----TATTATAAATCTTTTAAAGAAATATATACCTAAATAT 828  
Db 230 ---SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr 248  
QY 829 ACTAATATTGTGCAAAATACCTATAGAGAAGACTAAATAAATCTTGAAGACCACTAAT 888  
Db 249 ThrAspHisCysValAsnTrpTyrAsnValGlyLeuAsnSerLeuArgGlySerThrTyr 268  
QY 889 ATGAGATCGAGTATATTAATGATATATCGAGATATATGATCTATTACGTATTAGATACT 948  
Db 269 AspAlaTrpValLysPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeu 288  
QY 949 ATCGCTCAATTTTCTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGATAGGT 1008  
Db 289 IleValLeuPheProPheTyrAspValArgLeuTyrSerLys----- 302  
QY 1009 GGCATTAATCACTTACAGAGAAATTTATACACTGAAATTAATTTTGACGCTTT 1068  
Db 303 GlyValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheThrLeuAsn 321  
QY 1069 ACTTACCTTGAATTTCAACCAATCTCGCTATATATGGAATATATTTAACAGTTCAGGG 1128  
Db 322 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAsnSerIleArgLysPro--- 340  
QY 1129 CTGATGATTTTTCATTTTATGATCAACTTATATTTTATACAAA----- 1173  
Db 341 ---HisLeuPheAspTyrLeuArgGlyIleGluPheHisThrArgLeuArgProGlyTyr 359  
QY 1174 -----AATGAACGTACGGGAATCGTTGATTTGTTGATTCGGAATCGT 1215  
Db 360 SerGlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg 376  
QY 1216 AATGATCTACTTATGCTACGACGAAGTGAATATATATATGGAAGAACAGGTCCA 1275  
Db 377 ProSerIleGlySerAsnAspThrIleThrSerProPheTyrGlyAspLysSerIleGlu 396  
QY 1276 CCCACACAAACAACTTAAATCACTTGAATCCTATAAAGTTTCAATTTGTAACGTATGATA 1335  
Db 397 ProIleGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg 410  
QY 1336 CAAGTA-----ACTGCTACTTCCCTTTTCTTAAC-----ATATCTTTCAATTAAT 1383  
Db 411 ThrIleAlaAsnThrAspIleAlaPheProAspGlyLysIleTyrPheGlyValThr 430  
QY 1384 CAATTTGAATTTTAAATTAATTTCACTAGTAATAATTA-----ACATATCA 1434  
Db 431 LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp 450  
QY 1435 GCT-----GGGGGAATTTTATCTAATGATAAA-----AAA 1464  
Db 1464

Db 451 SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProProGlu 470  
QY 1465 ACACTGATTTTCAATTTCTGTAAATAAAGACTGTAAACCAATATTAAATCCAAATGTT 1524  
Db 471 ThrThrAsp-----GluProLeuGluLys----- 478  
QY 1525 TTACCAAGCTATATAGTATAGTATATTTATATCCAGCTTTTCTTTTAAATTTATTTCC 1584  
Db 479 -----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGln 493  
QY 1585 TATAAATGATAGTAGCGCTAAATATATATATATATACAGGTGATAGATGACACACAGT 1644  
Db 494 AspArgArgGlyThrIle-----ProPhePheThr-----TyrThrHisArg 507  
QY 1645 AGTCTTAAAGAAATATGCAATATATCAGATAAATAATATCAATGATCCAGCAATCAAA 1704  
Db 508 SerValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValLys 527  
QY 1705 GGTAACAGTCTTGATACAAACTCTAAGTAATCAAGGACCTGCTCATACAGGAGGAAAC 1764  
Db 528 AlaTyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsn 547  
QY 1765 TTGCTTTTATTACAA-----AGTCAAGGGCGTTTGAAGATTACAGTAGTAAGT 1812  
Db 548 LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer 567  
QY 1813 CCTAATTTCTACAACTTATTATAGCTTTCGATACGCTACAAATGCTGCTGGAAT 1872  
Db 568 AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 583  
QY 1873 ACTCTCTAATATATCTCTTCAATACACAGGAGTAAATAGGAATACCACTCAACGACTC 1932  
Db 584 -----ThrAsnLeuArgLeuPheVal-----GlnAsnSer 593  
QY 1933 AACAACTTTTCTGTACAAATTTAATAATTTTACAATAC-----GGAGATTTTGGG 1986  
Db 594 AsnAsnAspPheLeuValIleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 613  
QY 1987 TAT-----TTCCAATTTCCAAGTACAGTACATACCTTTAAATCGAAACATACCATTT 2040  
Db 614 TyrGlnThrPheAspPheAlaThrSer-----AsnSerAsnMetGlyPhe 628  
QY 2041 ATATTTAATCTGTCAGAT-----GTATCAAAATTTCAATTTTA 2076  
Db 629 SerGlyAspThrAsnAspPheIleIleGlyAlaGluSerPheValSerAsnGluLysIle 648  
QY 2077 ATCATGATAAAATTTGAATTTTATACCAATT 2106  
Db 649 TyrIleAspLysIleGluPheIleProVal 658  
RESULT 12  
US-09-427-770-112  
; Sequence 112, Application US/09427770  
; Patent No. 6620988  
; GENERAL INFORMATION:  
; APPLICANT: English, Leigh H.  
; APPLICANT: Brusock, Susan M.  
; APPLICANT: Malvar, Thomas W.  
; APPLICANT: Bryson, James W.  
; APPLICANT: Kulesza, Caroline A.  
; APPLICANT: Walters, Frederick S.  
; APPLICANT: Slatin, Stephen L.  
; APPLICANT: Von Teresh, Michael A.  
; APPLICANT: Romano, Charles  
; TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED  
; TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA









## REFERENCE/DOCKET NUMBER: MRCO:151

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 110:

## SEQUENCE CHARACTERISTICS:

LENGTH: 652 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-996-441B-110

## Alignment Scores:

Pred. No.:	4.82e-55	Length:	652
Score:	700.00	Matches:	216
Percent Similarity:	44.58%	Conservative:	117
Best Local Similarity:	28.92%	Mismatches:	272
Query Match:	17.77%	Indels:	142
DB:	2	Gaps:	32

US-10-782-570-1 (1-2235) x US-08-996-441B-110 (1-652)

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QY 1 GTGAATCAAAATAATAAATGAATATGAGATATATCGAT-----TCAAAGAAATTTATCTTAT 57
DB 1 MetAenProAenAenArgSerGluHisAspThrIleLysValThrProAenSerGluLeu 20
QY 58 CCTTCTACAGAAATTTGATCATTTCTAGATACCTTTACACAAATATCCAAATCAACCA 117
DB 21 ProthrAen-----HisAenGlnTyrProLeuAlaAspAenProAenSerThr 36
QY 118 TTCAAAACACAAATTTACAAAGAGTGGCTCAATATGCTCAA--GGGAATACACAATAT 174
DB 37 LeuGluGluLeuAenTyrLysGluPheLeuArgMetThrGluAenSerSerThrGluVal 56
QY 175 GGTGATAATTCGAGACATTTGCTAGTCTGATACAAATTTGCT---GCAGTTAGTCAGGT 231
DB 57 LeuAenAen-----SerThrValLysAspAlaValGlyThrGly 69
QY 232 ACTATTGATCCGGTACTCTGTTAGCCGGTATAGTGGGCTCACTTCTATATCCGGACCG 291
DB 70 IleSerValValGlyGlnIleLeuGlyValValGly----- 81
QY 292 ATAGAATAAATAGTGGCTATAATAATCTTTTGGTACCCTAATCACTGTCTTTTGGGCC 351
DB 82 ValProPheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAspThrIleTyrPro 101
QY 352 CGGGGAGAACAGACAAACAGTAGTAGACAAATTTATTAATAAATGGGAGAAATTTTGT 411
DB 102 Ser-----AspAlaAspProTyrLysAlaPheMetAlaGlnValGluValLeuile 118
QY 412 GATACACCGTTAACAGAAAGCATAAAGCAGCTAAAGTTACAACTTTAGAGAGTTTAGA 471
DB 119 AspLysLysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGln 138
QY 472 CAATATTACAAAGCTATAATACAGCATTAGATGATCGAGAAATATAAAGAGACTACAA 531
DB 139 AenAenPheGluAspTyrValAenAlaLeuAenSerTyrLysLys----- 153
QY 532 GCTCCTGGATTACCAACCATCATCAGCATTTACAAAGCTGCTTGAAGCTTTAAATACGA 591
DB 154 -----ThrProLeuSerLeuArgSerLysArgSerGlnAenArgIleArgGluLeu 170
QY 592 TTTGAGAAATGTCACATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAACCTTAT 651
DB 171 PheSerGlnAlaGluSerHisPheArgAenSerMetProSerPheAlaValSerLysPhe 190
QY 652 AAAACGCTATTACTACTATTATTCGCAAGCTGCTTAATTTTCAATTTAAATTTATACAA 711
DB 191 GluValLeuPheLeuProThrTyrAlaGlnAlaAlaAenThrHisLeuLeuLeuLys 210
QY 712 CAAGGTGCTGAATTCGGCTGATGAATGGAATGCGAGATATACATCCTTTCACAAATGGAACCT 771
DB 211 AspAlaGlnValPheGlyGluGluTyrGlySer----- 222

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QY 772 AATGCTGGAACATCAGATGACTATTATAAACTTTTAAAGAAATATATACCTAAATATAGT 831
DB 223 SerGluAspValAlaGluPheTyrHisArgGlnLeuLysLeuThr---GlnGlnTyrThr 241
QY 832 AACTATTGTGCAATACCTATAGAGAAGGACTAAATAAATCTTCCGAAGAACCTAAATATG 891
DB 242 AspHisCysValAenTyrAsnValGluAenGlyLeuArgGlySerThrTyrAsp 261
QY 892 AGATGGAGTATATTTAATGATTTATCGAAGATATATGACTATTACTGTATTAGATATATC 951
DB 262 AlaTyrValLysPheAenArgPheArgGluMetThrLeuThrValLeuAspLeuile 281
QY 952 GCTCAATTTCTTTTATGATATAAGAGAGATACAAAGATTCAATAGGAAGAAATAGGTGGC 1011
DB 282 ValLeuPheProPheTyrAspValArgLeuTyrSerLys-----Gly 295
QY 1012 ATTAAATCTGAATTTACAAGAAATTTATACAACTGAATATAAATTTTGACCGTCTTACT 1071
DB 296 ValLysThrGluLeuThrArgAspIlePheThrAspProIle---PheSerLeuAenThr 314
QY 1072 TACCTTGAATTTCAACCAATCTCGCTATATATGAATATATATTTAAACACGTTTCAGGGCT 1131
DB 315 LeuGlnGluTyrGlyProThrPheLeuSerIleGluAenSerIleArgLysPro----- 332
QY 1132 AGATTATTTTTCATTTTAGATGAATCTTATATTTTATACAAA----- 1173
DB 333 HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrSer 352
QY 1174 -----AATGAACGTCACGGGAATCGTTTAGTTAGTTATTCGGAATCGTAAT 1218
DB 353 GlyLysAspSerPheAenTyrTyrSerGlyAenTyr-----ValGluThrArgPro 369
QY 1219 AGATCTACTATGTCACGAGGAACCTGAATATATATATATATGAGAGAAGACAGGTCCACCC 1278
DB 370 SerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGluPro 389
QY 1279 ACAACAAACCTTTAAATACCAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCT 1338
DB 390 ValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----ArgThr 403
QY 1339 GTA-----ACTCTACTTCCCTTTTCTTAAC-----ATATACTTTTCAATTAATCAA 1386
DB 404 IleAlaAenThrAspValAlaAlaTyrProAenGlyLysIleTyrPheGlyValThrLys 423
QY 1387 ATTGAACCTTTATTAATAATTTACCTAGTATTAATAATTA-----ACATATTCACT 1437
DB 424 ValAspPheSerGlnTyrAspAspGlnLysAenGluThrSerThrGlnThrTyrAspSer 443
QY 1438 -----GGGGGAATTTATCTTAATGATAAA-----AAAAACA 1467
DB 444 LysArgAenAenGlyHisValGlyAlaGlnAenSerIleAspGlnLeuProGluThr 463
QY 1468 ACTGATTTTCAATTTCTGTAAATAAAGACGTGTAACCAATTTATTAATTTCAAAATTTGTTA 1527
DB 464 ThrAsp-----GluProLeuGluLys----- 470
QY 1528 CCAAGCTATATATGTTATGATCATATTTATCCAGCTTTTCTTTTATTTATTTATTTTCTAT 1587
DB 471 -----AlaTyrSerHisGlnLeuAenTyrAlaGluCysPheLeuMetGlnAsp 486
QY 1588 AAAATTGATTTAGCGCTAAATATATATATATATATAGTCAGTCATTAGGATGACACACAGTAGT 1647
DB 487 ArgArgGlyThrIle-----ProPhePheThr-----TyrThrHisArgSer 500
QY 1648 GTTAATAGAAATAATCAATATCAGATAAATAAATTAATTAATCAATGATCCCAAGCAATCAAGGT 1707
DB 501 ValAspPhePheAenThrIleAspAlaGluLysIleThrGlnLeuProValValLysAla 520
QY 1708 AACAGTCTTGATACAACTCTAAGGTAAATTCGAAGACCTGCTCATACAGGAGGAACCTTG 1767
DB 521 TyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAenLeu 540

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QY 892 AGATGGAGTATATTAATGATTATTCGAAGATATATGACTATTACTGTATTAGATATATC 951
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
262 AlaIrpVallylsPheAsnArgPheArgGluMetThrLeuThrValLeuAspLeuIle 281
QY 952 GCTCAATTTCTTTTATGATTAAGAGATACAAAGATTCAATAGGAGAAATAGGTGGC 1011
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
282 ValLeuPheProPheTyrAspValArgLeuTyrSerIys-----Gly 295
QY 1012 ATTAAACCTGAACTTACAGAGAAATTTATCAACTGAAATAAATTTTGACCGCTTACT 1071
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
296 VallysThrGluLeuThrArgAspIlePheThrAspProIle----PheSerLeuAsnThr 314
QY 1072 TACCTTGAAATTCACACCAATCTCGTATATGGAATATAATTTAAACAGTCGTGAGGCTT 1131
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
315 LeuGlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro----- 332
QY 1132 AGATTATTTTCATTTTATAGTGAATTTATATATTTTATATACAAA----- 1173
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
333 HisLeuPheAspTyrLeuGlnGlyIleGluPheHisThrArgLeuGlnProGlyTyrSer 352
QY 1174 -----AATGAACGTACCGGAATCGTTTGTGTTAGTTGCGAATCGTAAT 1218
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
353 GlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArgPro 369
QY 1219 AGATCTACTATGCTACGACAGGAAGTCAAAATATATATGAGAGAAAGACAGGTCCACCC 1278
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
370 SerIleGlySerSerLysThrIleThrSerProPheTyrGlyAspLysSerThrGluPro 389
QY 1279 ACAACAAAACTTTATACCAATTTGAACTCTATATAAGTTTCAATTTGTAATCATGATACAA 1338
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
390 ValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----ArgThr 403
QY 1339 GTA-----ACTCTACTTCCCTTTTCTCTAAC-----ATATACTTTCAATTAATCAA 1386
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
404 IleAlaAsnThrAspValAlaIatrpProAsnGlyLysIleTyrPheGlyValThrLys 423
QY 1387 ATTGAACCTTTATTAATAATTTCACTAGTATAATAATTA-----ACATATTCAGCT 1437
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
424 ValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAspSer 443
QY 1438 -----GGGGGGAATTTATCTAATGATAAA-----AAAACA 1467
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
444 LysArgAsnAsnGlyHisValGlyAlaGlnAspSerIleAspGlnLeuProGluThr 463
QY 1468 ACTGATTTTCAATTTCTGTAATAAAAGACTGTAACCAATTTAATCCAAATTTGTTA 1527
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
464 ThrAsp-----GluProLeuGluLys----- 470
QY 1528 CCAAGCTATAATAGTTATAGTATATTTATCCAGTTTCTTTATTTAATTTATCTTAT 1587
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
471 -----AlaTyrSerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAsp 486
QY 1588 AAAATTTGGATTAGCGCTAAATATATATATACAGGTGCAATAGGATGGACACACAGTAGT 1647
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
487 ArgArgGlyThrIle-----ProPhePheThr-----TrpThrHisArgSer 500
QY 1648 GTTAATAGAAATAATGCAATATCAGATAAAATAATATACATGATCCAGCAATCAAAGGT 1707
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
501 ValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValVallysAla 520
QY 1708 AACAGCTCTTGATCAAACTCTAAGGTAATTTGAAGCACTGTCATACAGGAGGAACTTGG 1767
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
521 TyrAlaLeuSerSerGlyAlaSerIleIleGluGlyProGlyPheThrGlyGlyAsnLeu 540
QY 1768 GTTTATTATTACAA-----AGTCAAGGCGGTTTAGAGATTTACATGTAGAACTCCT 1815
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
541 LeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSerAla 560
QY 1816 AATTCTACACAATCTTTATTTACATTTAGACTTCGATACGCTACAAATGGTCTGGAATACT 1875
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
561 AlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr----- 575
QY 1876 CTTCTCAATATATCTCTTACATACCAGGNGTAAATAGGAATACCACCTCAACGACTCAAC 1935
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Db ||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
576 ---ThrAsnLeuArgLeuPheVal-----GlnAsnSerAsn 586
QY 1936 AACACTTTTCTGTACAAATTTATAATAATTATTACAATAC-----GGAGATTTTGGGTAT 1989
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
587 AsnAspPheIleValIleTyrIleAsnLysThrMetAsnIleAspAspLeuThrTyr 606
QY 1990 TTCCAATTTCCAGTACACAGTAAACATTACCTTTTAAATCGAAACATACCATTT----- 2040
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
607 GlnThrPheAspLeuAlaThrThr-----AsnSerAsnMetGlyPheSerGlyAsp 623
QY 2041 -----ATATTTAATCGTGCAGATGTATCAAAATTTTCAATTTTATCATTCAT 2085
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
624 ThrAsnGluLeuIleIleGlyAlaGluSerPheValSerAsnGluLysIleTyrIleAsp 643
QY 2086 AAAATTCGAAATTTATACCAATTT 2106
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644 LysIleGluPheIleProVal 650
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Job time : 88 secs

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